

CONTIG4950	16836505_c2_9	5745	19848	435	145	YKR026C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ykr026c] [pn:translation initiation factor eif2b, 34 kd, alpha subunit:translation initiation factor eif-2b alpha subunit:eif-2b gdp-gip exchange factor:guanine nucleotide exchange factor subunit gen3:gcd complex subunit gen3:trans
CONTIG5254	24113537_c3_24	5746	19849	528	176	YKR084C	455	3.6(10)-43	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbsl:ykr404] [gctc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5254	4375703_c3_23	5747	19850	711	237	YKR084C	154	2.1(10)-9	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbsl:ykr404] [gctc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5254	4100936_c3_22	5748	19851	423	141	YKR084C	115	5.2(10)-6	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbsl:ykr404] [gctc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG989	56_f1_1	5749	19852	597	199	YKR084C	176	1.5(10)-12	Saccharomyces cerevisiae	[ui:yrk084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbs1.ykr404] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3453	1562_c1_6	5750	19853	1317	439	YLR249W	1265	5.2(10)-129	Saccharomyces cerevisiae	[ui:ylr249w] [pn:translation elongation factor eef3:elongation factor 3:eef-3] [gn:yeB3:efc1:i9672] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3994	132962_c3_10	5751	19854	564	188	YLR249W	690	1.5(10)-67	Saccharomyces cerevisiae	[ui:ylr249w] [pn:translation elongation factor eef3:elongation factor 3:eef-3] [gn:yeB3:efc1:i9672] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3994	1288135_c3_9	5752	19855	234	78	YLR249W	138	3.6(10)-8	Saccharomyces cerevisiae	[ui:ylr249w] [pn:translation elongation factor eef3:elongation factor 3:eef-3] [gn:yeB3:efc1:i9672] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4952	25636466_f2_2	5753	19856	1782	594	YLR289W	1866	1.1(10)-192	Saccharomyces cerevisiae	[ui:ylr289w] [pn:strong similarity to e. coli elongation factor-type gtp-binding protein lepa:gtp-binding protein:gpase] [gn:gu1] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]



CONTIG5506	21969677_13_6	5754	19857	1128	376	YLR291C	902	1.6(10)-90	Saccharomyces cerevisiae	[ui:ylr291c] [pn:translation initiation factor eif2b, 43 kda subunit:translation initiation factor eif-2b gamma subunit:eif-2b gdp-glp exchange factor:guanine nucleotide exchange factor subunit gcd7,gcd complex subunit gcd7] [gn:gcd7:1]
CONTIG5782	36504568_c3_24	5755	19858	906	302	YMR146C	858	7.2(10)-86	Saccharomyces cerevisiae	[ui:ymr146c] [pn:translation initiation factor eif3, p39 subunit:translation initiation factor eif-3 p39 subunit] [gn:tf34:ym9375] [gicfc:10.7] [kegfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5466	4566_c3_16	5756	19859	507	169	YMR260C	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:ymr260c] [pn:translation initiation factor eif1a,eukaryotic initiation factor 1a:eif-1a:eif-4c] [gn:tif1:ym8156] [gicfc:10.7] [kegfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4683	16281457_c3_5	5757	19860	1890	630	YMR309C	1048	5.2(10)-106	Saccharomyces cerevisiae	[ui:ymr309c] [pn:associated with 40s ribosomal subunit:nuclear transport protein nip1] [gn:nip1:ym9924] [gicfc:10.4:10.7:10.1:12.6] [kegfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG959	6325_12_2	5758	19861	351	117	YNL244C	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:ynl244c] [pn:translation initiation factor 3:eif3:protein translation factor sui1] [gn:sui1:rf1:n0905] [gicfc:10.7] [kegfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG4356	10969075_f1_1	5759	19862	1965	655	YNL163C	919	1.8(10)-110	Saccharomyces cerevisiae	[ui:ynl163c] [pn:translation elongation factor eef4:hyposhical 124.5 kd protein in sko1-rpl44a intergenic region] [gn:n1718] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
blx18355.x	14554563_c3_3	5760	19863	483	161	YNL163C	502	4.9(10)-47	Saccharomyces cerevisiae	[ui:ynl163c] [pn:translation elongation factor eef4:hyposhical 124.5 kd protein in sko1-rpl44a intergenic region] [gn:n1718] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1921	33375286_f1_1	5761	19864	246	82	YNL062C	165	1.5(10)-11	Saccharomyces cerevisiae	[ui:ynl062c] [pn:translation initiation factor eif3 rna-binding subunit:gcd10 protein] [gn:gcd10:n2422] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3550	35283312_f2_1	5762	19865	948	316	YNL062C	616	3.2(10)-60	Saccharomyces cerevisiae	[ui:ynl062c] [pn:translation initiation factor eif3 rna-binding subunit:gcd10 protein] [gn:gcd10:n2422] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1531	31808333_f3_2	5763	19866	984	328	YNL014W	1377	7.2(10)-141	Saccharomyces cerevisiae	[ui:ynl014w] [pn:translation elongation factor eef3 homolog:putative elongation elongation factor 3 homolog:eef-3] [gn:n2846] [gtcf:10.7:12.6] [keggfc:14.2] [sgdfc:5.2.0.7.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3994	14628192_c2_7	5764	19867	354	118	YNL014W	429	2.8(10)-39	Saccharomyces cerevisiae	[ui:ynl014w] [pn:translation elongation factor eef3 homolog:putative elongation elongation factor 3 homolog:ef-3] [gn:n2846] [gctc:10.7:12.6] [kegfc:14.2] [sgdfe:5.2:0.7:9.0] [db:gic-saccharomyces cerevisiae]
CONTIG3078	5312510_c2_6	5765	19868	1122	374	YOL139C	120	2.0(10)-5	Saccharomyces cerevisiae	[ui:yol139c] [pn:translation initiation factor eif4e:eukaryotic binding protein] [gn:itf45:cde33] [gctc:10.7] [kegfc:14.2] [sgdfe:5.2:0.9:2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4733	25476625_f2_4	5766	19869	669	223	YOL139C	583	9.9(10)-57	Saccharomyces cerevisiae	[ui:yol139c] [pn:translation initiation factor eif4e:eukaryotic binding protein] [gn:itf45:cde33] [gctc:10.7] [kegfc:14.2] [sgdfe:5.2:0.9:2.0] [db:gic-saccharomyces cerevisiae]
b3x16009.y	14095287_f1_1	5767	19870	270	90	YOL139C	230	2.5(10)-19	Saccharomyces cerevisiae	[ui:yol139c] [pn:translation initiation factor eif4e:eukaryotic binding protein] [gn:itf45:cde33] [gctc:10.7] [kegfc:14.2] [sgdfe:5.2:0.9:2.0] [db:gic-saccharomyces cerevisiae]

CONTIG2719	35803130_f3_2	5768	19871	855	285	YOR260W	303	1.5(10)-38	Saccharomyces cerevisiae	[ui:yor260w] [pn:translation initiation factor eif2bgamma subunit:translation initiation factor eif-2b gamma subunit:eif-2b gdp-glp exchange factor:guanine nucleotide exchange factor subunit gcd1:gcd complex subunit gcd1] [gn:gcd1:tra3]
CONTIG3491	26604767_f2_5	5769	19872	459	153	YOR260W	172	1.1(10)-15	Saccharomyces cerevisiae	[ui:yor260w] [pn:translation initiation factor eif2bgamma subunit:translation initiation factor eif-2b gamma subunit:eif-2b gdp-glp exchange factor:guanine nucleotide exchange factor subunit gcd1:gcd complex subunit gcd1] [gn:gcd1:tra3]
CONTIG3568	19943775_f3_1	5770	19873	546	182	YOR276W	161	5.2(10)-12	Saccharomyces cerevisiae	[ui:yor276w] [pn:mma cap-binding protein:eif4f, 20k subunit:20 kd cap associated protein] [gn:ca20:cap20] [gtcf:10.7] [kegfc:14.2] [sgdfc:5.2,0;9.2,0] [db:gic-saccharomyces cerevisiae]
CONTIG4524	10156507_c2_6	5771	19874	927	309	YOR361C	402	1.3(10)-54	Saccharomyces cerevisiae	[ui:yor361c] [pn:translation initiation factor eif3 subunit:cell cycle regulation and translation initiation protein] [gn:prt1:cdc63] [gtcf:10.7;12.8] [kegfc:14.2] [sgdfc:3.8,0;5.2,0;9.2,0] [db:gic-saccharomyces cerevisiae]

CONTIG3920	25478412_12_1	5772	19875	858	286	YPL237W	693	2.2(10)-68	Saccharomyces cerevisiae	[ui:yp1237w] [pn:translation initiation factor eif2 beta subunit:translation initiation factor 2 beta subunit:eif-2-beta] [gn:sui3] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5642	23915932_12_3	5773	19876	3591	1197	YPL226W	3359	0	Saccharomyces cerevisiae	[ui:yp1226w] [pn:similarity to translation elongation factor eef3] [gtcf:10.7:12.6] [keggfc:14.2] [sgdfc:5.2.0:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4304	23478550_c3_9	5774	19877	585	195	YPL048W	310	8.4(10)-28	Saccharomyces cerevisiae	[ui:yp1048w] [pn:translation elongation factor eef1 alpha chain:elongation factor 1-gamma 1:eif-1-gamma 1] [gn:tef3:cam1] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4304	4297162_c2_8	5775	19878	234	78	YPL048W	186	5.5(10)-14	Saccharomyces cerevisiae	[ui:yp1048w] [pn:translation elongation factor eef1 alpha chain:elongation factor 1-gamma 1:eif-1-gamma 1] [gn:tef3:cam1] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4885	7308137_c1_9	5776	19879	1170	390	YPL048W	713	1.0(10)-96	Saccharomyces cerevisiae	[ui:yp1048w] [pn:translation elongation factor eef1 alpha chain:elongation factor 1-gamma 1:eif-1-gamma 1] [gn:tef3:cam1] [gtcf:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2323	4303191_f2_1	5777	19880	1089	363	YPR041W	537	4.5(10)-84	Saccharomyces cerevisiae	[ui:yp041w] [pn:translation initiation factor eif5:eukaryotic initiation factor 5:eif-5] [gn:tif5:yp3085] [gctc:10.7] [kegfc:14.2] [sgdfc:5.2:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG182	29376640_f2_2	5778	19881	756	252	YPR041W	303	4.2(10)-41	Saccharomyces cerevisiae	[ui:yp041w] [pn:translation initiation factor eif5:eukaryotic initiation factor 5:eif-5] [gn:tif5:yp3085] [gctc:10.7] [kegfc:14.2] [sgdfc:5.2:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1738	5207026_f3_3	5779	19882	948	316	YPR163C	344	2.1(10)-31	Saccharomyces cerevisiae	[ui:yp163c] [pn:translation initiation factor eif4b:translation initiation factor tif3:stim1:eif-4b] [gn:tif3:stim1:p9325] [gctc:10.7] [kegfc:14.2] [sgdfc:5.2:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3827	24697182_f3_3	5780	19883	867	289	YFR009W	893	1.3(10)-89	Saccharomyces cerevisiae	[ui:yfr009w] [pn:positive effector of gen2p:protein] [gn:gen20] [gctc:10.7:12.6] [kegfc:14.2] [sgdfc:5.3:0:7.9:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3827	6843955_f3_4	5781	19884	1026	342	YFR009W	1247	4.2(10)-127	Saccharomyces cerevisiae	[ui:yfr009w] [pn:positive effector of gen2p:protein] [gn:gen20] [gctc:10.7:12.6] [kegfc:14.2] [sgdfc:5.3:0:7.9:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2245	5913393_f1_1	5782	19885	897	299	YGL195W	597	1.8(10)-56	Saccharomyces cerevisiae	[ui:ygl195w] [pn:translational activator:translational activator gen1] [gn:gen1:g1318] [gctc:10.7] [kegfc:14.2] [sgdfc:5.3:0:9.2:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4938	24787825_f1_3	5783	19886	1338	446	YGL195W	193	1.0(10)-23	Saccharomyces cerevisiae	[ui:yg1195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:g1318] [gtcf:10.7] [kegfc:14.2] [sgdfe:5.3:0.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5175	15663535_c2_9	5784	19887	3177	1059	YGL195W	1442	1.3(10)-235	Saccharomyces cerevisiae	[ui:yg1195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:g1318] [gtcf:10.7] [kegfc:14.2] [sgdfe:5.3:0.9.2.0] [db:gic-saccharomyces cerevisiae]
b9x13s54.x	23955187_f2_1	5785	19888	363	121	YGL195W	172	2.0(10)-14	Saccharomyces cerevisiae	[ui:yg1195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:g1318] [gtcf:10.7] [kegfc:14.2] [sgdfe:5.3:0.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG2020	10976532_f1_1	5786	19889	900	300	YJL125C	655	2.2(10)-64	Saccharomyces cerevisiae	[ui:yj1125c] [pn:translational repressor of gcn4:gcd14 protein] [gn:gcd14:j0710] [gtcf:10.7] [kegfc:14.2] [sgdfe:5.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3643	782750_f3_2	5787	19890	549	183	YMR028W	151	3.8(10)-14	Saccharomyces cerevisiae	[ui:ymr028w] [pn:component of the for signaling pathway] [gn:tap42] [gtcf:12.13] [kegfc:14.2] [sgdfe:3.8:0.5.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2486	22926268_f2_2	5788	19891	981	327	YNL139C	114	0.0015	Saccharomyces cerevisiae	[ui:ynl139c] [pn:regulatory protein:rtf1 protein] [gn:rtf1:n1209:n1835] [gtcf:10.7] [kegfc:14.2] [sgdfe:5.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3826	4489075_c3_4	5789	19892	1431	477	YNL139C	234	4.5(10)-16	Saccharomyces cerevisiae	[ui:ynl139c] [pn:regulatory protein:rtf1 protein] [gn:rtf1:n1209:n1835] [gtcf:10.7] [kegfc:14.2] [sgdfe:5.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG2848	964062_f1_1	5790	19893	555	185	YGR147C	151	1.5(10)-10	Saccharomyces cerevisiae	[ui: ygr147c] [pn: n-acetyltransferase for n-terminal methionine: n-terminal acetyltransferase 2: amino-terminal, alpha-amino, acetyltransferase 2] [gn: na2.g6630] [gctc: 10.7:14.1] [ec: 2.3.1.88] [keggfc: 14.1] [sgdfc: 5.5:0:6.3:0:9:2.0] [d
CONTIG5076	1206562_c1_7	5791	19894	465	155	YHR189W	184	1.8(10)-14	Saccharomyces cerevisiae	[ui: yhr189w] [pn: similarity to peptidyl-trna hydrolases: putative peptidyl-trna hydrolase: pth] [gctc: 10.7] [ec: 3.1.1.29] [keggfc: 14.1] [sgdfc: 5.5:0] [db: gtc-saccharomyces cerevisiae]
CONTIG1050	24303779_c1_2	5792	19895	621	207	YHR189W	243	1.1(10)-20	Saccharomyces cerevisiae	[ui: yhr189w] [pn: similarity to peptidyl-trna hydrolases: putative peptidyl-trna hydrolase: pth] [gctc: 10.7] [ec: 3.1.1.29] [keggfc: 14.1] [sgdfc: 5.5:0] [db: gtc-saccharomyces cerevisiae]
CONTIG3262	4942012_c2_6	5793	19896	1119	373	YMR005W	234	5.7(10)-34	Saccharomyces cerevisiae	[ui: ymr005w] [pn: required for protein synthesis: mpt1 protein] [gn: mpt1.ym8270] [gctc: 10.7] [keggfc: 14.2] [sgdfc: 5.5:0] [db: gtc-saccharomyces cerevisiae]
CONTIG3952	14260931_c3_7	5794	19897	1650	550	YNL209W	2231	2.2(10)-231	Saccharomyces cerevisiae	[ui: ynl209w] [pn: heat shock protein of hsp70 family, cytosolic: heat shock protein ssb2] [gn: ssb2.n1333] [gctc: 12.7] [keggfc: 14.2] [sgdfc: 5.5:0:9:2.0] [db: gtc-saccharomyces cerevisiae]



CONTIG5378	20319182_c2_15	5795	19898	543	181	YBR164C	708	5.5(10)-70	Saccharomyces cerevisiae	[ui:ybr164c] [pn:adp-ribosylation factor:adp-ribosylation factor-like protein 1] [gn:arl1:arl3:ybr1216] [gicfc:10.7:12.10] [keggfc:14.2] [sgdfe:6.3:0:8.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5109	4103506_f1_1	5796	19899	720	240	YDL212W	314	3.2(10)-28	Saccharomyces cerevisiae	[ui:ydl212w] [pn:endoplasmic reticulum membrane protein:secretory component protein] [gn:shr3] [gicfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfe:6.2:0:6.3:0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5715	24022191_c1_10	5797	19900	801	267	YDR098C	676	1.3(10)-66	Saccharomyces cerevisiae	[ui:ydr098c] [pn:similarity to legionella glutaredoxin-like protein] [gicfc:10.7] [keggfc:14.2] [sgdfe:6.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5792	20120390_f2_9	5798	19901	2463	821	YDR495C	103	0.11	Saccharomyces cerevisiae	[ui:ydr495c] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps3] [gn:vps3:d9719] [gicfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfe:6.2:0:6.3:0:6.4:0:9.10.0] [db:gic-saccharomyces cerevisiae]

CONTIG4598	14879155_fl_1	5799	19902	579	193	YEL012W	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:ye1012w] [pn:ubiquitin-conjugating enzyme e2-24 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc8] [gtcf:10.7] [ec:6.3.2.19] [kegcf:14.1] [sgdfe:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5659	11719175_f3_11	5800	19903	1395	465	YER005W	1212	2.2(10)-123	Saccharomyces cerevisiae	[ui:yer005w] [pn:similarity to gda1p:hypothetical 71.9 kd protein in pmi40-pac2 intergenic region] [gtcf:10.7] [kegcf:14.2] [sgdfe:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5659	4882788_f3_12	5801	19904	801	267	YER005W	121	8.5(10)-5	Saccharomyces cerevisiae	[ui:yer005w] [pn:similarity to gda1p:hypothetical 71.9 kd protein in pmi40-pac2 intergenic region] [gtcf:10.7] [kegcf:14.2] [sgdfe:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG225	32032160_c3_2	5802	19905	327	109	YGI203C	103	0.00012	Saccharomyces cerevisiae	[ui:ygi203c] [pn:carboxypeptidase:ysc-alpha:carboxypeptidase precursor:carboxypeptidase d] [gn:kex1] [gtcf:10.7:12.16] [ec:3.4.16.6] [kegcf:14.1] [sgdfe:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5562	22456555_c1_8	5803	19906	1578	526	YGL203C	971	7.5(10)-98	Saccharomyces cerevisiae	[ui:yg1203c] [pn:carboxypeptidase:ysc-alpha:carboxypeptidase precursor:carboxypeptidase d] [gn:kex1] [gtcf:10.7:12.16] [ec:3.4.16.6] [kegfc:14.1] [sgdfc:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5531	4354803_c3_34	5804	19907	570	190	YGR133W	276	3.3(10)-24	Saccharomyces cerevisiae	[ui:ygr133w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-21 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:pas2:ubc10] [gtcf:10.7:12.16:12.6] [ec:6.3.2.19] [kegfc:14.1] [sgdfc:6.3.0:6.4.0:9.8.0] [db
CONTIG4597	19584530_f1_1	5805	19908	378	126	YGR209C	126	2.6(10)-8	Saccharomyces cerevisiae	[ui:ygr209c] [pn:thioredoxin ii:thioredoxin i:r-i] [gn:trx2:trx1:g7746] [gtcf:10.7:12.12:12.8] [kegfc:14.2] [sgdfc:3.8.0:6.3.0:1.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5028	10979805_f3_6	5806	19909	990	330	YGR209C	194	3.2(10)-15	Saccharomyces cerevisiae	[ui:ygr209c] [pn:thioredoxin ii:thioredoxin i:r-i] [gn:trx2:trx1:g7746] [gtcf:10.7:12.12:12.8] [kegfc:14.2] [sgdfc:3.8.0:6.3.0:1.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5804	22689062_f1_11	5807	19910	1473	491	YJR117W	1227	5.7(10)-125	Saccharomyces cerevisiae	[ui:ylr117w] [pn:zinc metallo-protease:hypothetical 52.3 kd protein in nrf1-atp2 intergenic region] [gn:ste24;j2032] [gtcf:10.11:12.9] [keggfc:14.2] [sgdfc:3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2164	1300_c2_3	5808	19911	330	110	YLR043C	332	3.8(10)-30	Saccharomyces cerevisiae	[ui:ylr043c] [pn:thioredoxin i:thioredoxin ii:tr-ii] [gn:trx1:trx2] [gtcf:10.7.12.12:12.8] [keggfc:14.2] [sgdfc:3.8.0:6.3.0.11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3792	6095437_c1_10	5809	19912	627	209	YLR066W	403	1.2(10)-37	Saccharomyces cerevisiae	[ui:ylr066w] [pn:similarity to signal peptidase] [gtcf:11.1] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1309	31645177_c2_4	5810	19913	1179	393	YLR121C	144	5.2(10)-7	Saccharomyces cerevisiae	[ui:ylr121c] [pn:strong similarity to aspartyl/proteases] [gtcf:10.11:5.2] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
b2x10323.y	7219712_f3_1	5811	19914	477	159	YLR244C	616	3.2(10)-60	Saccharomyces cerevisiae	[ui:ylr244c] [pn:methionine aminopeptidase, isoform 1:methionine aminopeptidase 1 precursor:metap 1:peptidase m 1:map] [gn:map1:j9672] [gtcf:10.7.14.1] [ec:3.4.11.18] [keggfc:14.1] [sgdfc:6.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2489	11907537_f1_3	5812	19915	465	155	YLR389C	143	1.0(10)-8	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcf:10.11:12.9] [keggfc:14.2] [sgdfc:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5476	21523515_f3_7	5813	19916	1077	359	YLR389C	790	1.1(10)-78	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcf:10.11:12.9] [keggfc:14.2] [sgdfe:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5476	33396075_f2_5	5814	19917	2469	823	YLR389C	1272	9.5(10)-130	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcf:10.11:12.9] [keggfc:14.2] [sgdfe:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG882	4509775_f1_1	5815	19918	819	273	YLR389C	313	6.7(10)-27	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcf:10.11:12.9] [keggfc:14.2] [sgdfe:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5196	13671877_f1_2	5816	19919	573	191	YML055W	189	5.5(10)-15	Saccharomyces cerevisiae	[ui:yml055w] [pn:signal peptidase 18 kd subunit] [gn:spc2] [gtcf:11.1:10.7:12.16] [keggfc:14.2] [sgdfe:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3894	14063427_c2_7	5817	19920	1125	375	YMR152W	305	2.8(10)-27	Saccharomyces cerevisiae	[ui:ymr152w] [pn:mitochondrial inner membrane protease:hypothetical 41.6 kd protein in imp1-hlj1 intergenic region:rf1095] [gn:ym9375] [gtcf:10.11:12.16] [keggfc:14.2] [sgdfe:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5708	23469680_f1_9	5818	19921	1089	363	YMR152W	248	6.7(10)-20	Saccharomyces cerevisiae	[ui:ymr152w] [pn:mitochondrial inner membrane protease:hypothetical 41.6 kd protein in imp1-hlj1 intergenic region:rf1095] [gn:ym93751] [gctc:10.11:12.16] [keggfc:14.2] [sgdfe:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4441	995300_c3_5	5819	19922	840	280	YNL238W	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:ynl238w] [pn:endoproteinase of late golgi compartment:kexin precursor:kex2 protease:proteinase yscf] [gn:kex2.qds1.n1122] [gctc:10.11:12.16:12.9] [ec:3.4.21.61] [keggfc:14.1] [sgdfe:3.3.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevi
CONTIG5003	506693_f1_1	5820	19923	1191	397	YOR219C	226	8.9(10)-16	Saccharomyces cerevisiae	[ui:yor219c] [pn:type iv dipeptidyl aminopeptidase:dipeptidyl aminopeptidase a:dpap a:ysci v] [gn:ste13.ycel.yor50-9] [gctc:10.7:12.16:12.9] [ec:3.4.14.-] [keggfc:14.1] [sgdfe:3.3.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5003	24238387_f2_4	5821	19924	1581	527	YOR219C	958	1.8(10)-96	Saccharomyces cerevisiae	[ui:yor219c] [pn:type iv dipeptidyl aminopeptidase:dipeptidyl aminopeptidase a:dpap a:ysci v] [gn:ste13.ycel.yor50-9] [gctc:10.7:12.16:12.9] [ec:3.4.14.-] [keggfc:14.1] [sgdfe:3.3.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

b2x12432.y	980002_c3_10	5822	19925	459	153	YPL051W	161	5.2(10)-12	Saccharomyces cerevisiae	[ui:ypi051w] [pn:strong similarity to adp-ribosylation factors] [gtcf:10.7:12.10] [keggfc:14.2] [sgdfc:6.3:0:8.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3269	16485902_c3_2	5823	19926	1122	374	YPL050C	1025	1.3(10)-103	Saccharomyces cerevisiae	[ui:ypi050c] [pn:required for complex n-glycosylation:protein] [gn:mmn9] [gtcf:10.7:12.16] [keggfc:14.2] [sgdfc:6.3:0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5127	33477192_c3_10	5824	19927	465	155	YPR131C	394	1.1(10)-36	Saccharomyces cerevisiae	[ui:ypr131c] [pn:similarity to n-acetyltransferases] [gtcf:10.7] [keggfc:14.2] [sgdfc:6.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4781	23945177_c2_4	5825	19928	1926	642	YAL002W	254	7.5(10)-36	Saccharomyces cerevisiae	[ui:yal002w] [pn:vacuolar sorting protein, 134 kD: vacuolar protein sorting-associated protein vps8] [gn:vps8:fun15] [gtcf:10.7:11.1:12.13] [keggfc:14.2] [sgdfc:6.2:0:8.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4781	26368752_c2_3	5826	19929	804	268	YAL002W	188	2.6(10)-12	Saccharomyces cerevisiae	[ui:yal002w] [pn:vacuolar sorting protein, 134 kD: vacuolar protein sorting-associated protein vps8] [gn:vps8:fun15] [gtcf:10.7:11.1:12.13] [keggfc:14.2] [sgdfc:6.2:0:8.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5445	1194062_c1_9	5827	19930	1035	345	YBL017C	802	9.0(10)-79	Saccharomyces cerevisiae	[ui:yb017c] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1 precursor:vacuolar carboxypeptidase sorting receptor vps10:carboxypeptidase y receptor] [gn:pep1:vps10:yb0302:yb03] [gtcfc:10
CONTIG5445	15648387_c1_8	5828	19931	306	102	YBL017C	183	9.5(10)-13	Saccharomyces cerevisiae	[ui:yb017c] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1 precursor:vacuolar carboxypeptidase sorting receptor vps10:carboxypeptidase y receptor] [gn:pep1:vps10:yb0302:yb03] [gtcfc:10
CONTIG5445	19735877_c3_14	5829	19932	1089	363	YBL017C	466	7.0(10)-43	Saccharomyces cerevisiae	[ui:yb017c] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1 precursor:vacuolar carboxypeptidase sorting receptor vps10:carboxypeptidase y receptor] [gn:pep1:vps10:yb0302:yb03] [gtcfc:10



CONTIG3639	2835062_f2_2	5830	19933	738	246	YBR171W	341	4.4(10)-31	Saccharomyces cerevisiae	[ui:yr171w] [pn:er protein-translocation complex subunit:translocation protein sec6:hssl protein] [gn:sec6:hssl:sec71:yr1232] [gtcf:10.7:1.1:12.16:12.6] [kegfc:14.2] [sgdfc:6.2:0.7:11.0:8.8:0.9:4.0] [db:gic-saccharomyces cerevi]
CONTIG5674	897627_f3_10	5831	19934	1509	503	YBR283C	870	3.7(10)-87	Saccharomyces cerevisiae	[ui:yr283c] [pn:strong similarity to sec61p:hyposhetical 53.3 kd protein in mrp]37-ape3 intergenic region] [gn:yr2020] [gtcf:10.7:1.1:12.6] [kegfc:14.2] [sgdfc:6.2:0.17:0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3000	24022761_c2_5	5832	19935	975	325	YBR288C	180	1.1(10)-23	Saccharomyces cerevisiae	[ui:yr288c] [pn:clathrin-associated protein complex, medium subunit:adapin medium chain homolog apm3] [gn:apm3:yks6:yr2035] [gtcf:10.7:1.1:12.10:12.16] [kegfc:14.2] [sgdfc:6.2:0.8:3.0:9.9:0] [db:gic-saccharomyces cerevisiae]
CONTIG3000	1067626_c2_4	5833	19936	615	205	YBR288C	103	0.0028	Saccharomyces cerevisiae	[ui:yr288c] [pn:clathrin-associated protein complex, medium subunit:adapin medium chain homolog apm3] [gn:apm3:yks6:yr2035] [gtcf:10.7:1.1:12.10:12.16] [kegfc:14.2] [sgdfc:6.2:0.8:3.0:9.9:0] [db:gic-saccharomyces cerevisiae]

CONTIG5426	23546918_f2_4	5834	19937	630	210	YDR005C	205	4.0(10)-16	Saccharomyces cerevisiae	[ui:ydr005c] [pn:required for sorting of mod5p:mafi protein] [gn:mafi:ydr119] [gtcf:10.7:11.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG685	33707807_c1_1	5835	19938	495	165	YDR005C	207	2.3(10)-16	Saccharomyces cerevisiae	[ui:ydr005c] [pn:required for sorting of mod5p:mafi protein] [gn:mafi:ydr119] [gtcf:10.7:11.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1218	23828127_c3_7	5836	19939	405	135	YDR244W	303	2.7(10)-26	Saccharomyces cerevisiae	[ui:ydr244w] [pn:putative peroxisomal targeting signal receptor:peroxisomal targeting signal receptor:peroxisomal protein pas10:peroxin 5] [gn:pas10:pex5:ydr419] [gtcf:11.3:12.6:12.12] [keggfc:14.2] [sgdfe:6.2.0:8.4.0:9.8.0] [db:gtc-
CONTIG441	1988968_c3_7	5837	19940	867	289	YDR244W	402	3.0(10)-37	Saccharomyces cerevisiae	[ui:ydr244w] [pn:putative peroxisomal targeting signal receptor:peroxisomal targeting signal receptor:peroxisomal protein pas10:peroxin 5] [gn:pas10:pex5:ydr419] [gtcf:11.3:12.6:12.12] [keggfc:14.2] [sgdfe:6.2.0:8.4.0:9.8.0] [db:gtc-

CONTIG3841	19703135_f3_4	5838	19941	747	249	YDR323C	209	1.1(10)-27	Saccharomyces cerevisiae	[ui: ydr323c] [pn: vacuolar segregation protein: vac1 protein] [gn: vac1: pep7: vps19] [gtcf: 10.7: 1.1: 1.12.13: 12.16] [kegfc: 14.2] [sgdfc: 6.2: 0.8: 5.0: 9.10.0] [db: gtc-saccharomyces cerevisiae]
CONTIG4931	2128317_c1_10	5839	19942	219	73	YDR323C	154	2.6(10)-10	Saccharomyces cerevisiae	[ui: ydr323c] [pn: vacuolar segregation protein: vac1 protein] [gn: vac1: pep7: vps19] [gtcf: 10.7: 1.1: 1.12.13: 12.16] [kegfc: 14.2] [sgdfc: 6.2: 0.8: 5.0: 9.10.0] [db: gtc-saccharomyces cerevisiae]
CONTIG2910	19722192_c3_2	5840	19943	1179	393	YDR414C	152	2.7(10)-8	Saccharomyces cerevisiae	[ui: ydr414c] [pn: required for retention of luminal er proteins: erd1 protein] [gn: erd1: d9461] [gtcf: 10.7: 1.1: 1.12.16] [kegfc: 14.2] [sgdfc: 6.2: 0.9: 4.0] [db: gtc-saccharomyces cerevisiae]
CONTIG3698	21892017_f1_1	5841	19944	1401	467	YER101C	194	1.3(10)-12	Saccharomyces cerevisiae	[ui: yer101c] [pn: strong similarity to as1p: protein] [gn: as12] [gtcf: 10.7: 1.1: 1] [kegfc: 14.2] [sgdfc: 6.2: 0] [db: gtc-saccharomyces cerevisiae]
CONTIG2448	14725067_c2_3	5842	19945	1620	540	YGL206C	1665	2.2(10)-171	Saccharomyces cerevisiae	[ui: ygl206c] [pn: clathrin heavy chain] [gn: chcl] [gtcf: 10.7: 1.1: 1.12.6] [kegfc: 14.2] [sgdfc: 6.2: 0.8: 7.0: 9.2.0] [db: gtc-saccharomyces cerevisiae]

CONTIG2931	78182_c3_3	5843	19946	1176	392	YGI.206C	1386	8.0(10)-142	Saccharomyces cerevisiae	[ui:yg 206c] [pn:clathrin heavy chain] [gn:chc1] [gtcf:10.7:1.1:1:12.6] [keggfc:14.2] [sgdfc:6.2:0:8.7:0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3596	24697182_c1_6	5844	19947	825	275	YGI.206C	732	3.2(10)-71	Saccharomyces cerevisiae	[ui:yg 206c] [pn:clathrin heavy chain] [gn:chc1] [gtcf:10.7:1.1:1:12.6] [keggfc:14.2] [sgdfc:6.2:0:8.7:0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG390	5079805_f2_1	5845	19948	1143	381	YGI.206C	1280	1.3(10)-130	Saccharomyces cerevisiae	[ui:yg 206c] [pn:clathrin heavy chain] [gn:chc1] [gtcf:10.7:1.1:1:12.6] [keggfc:14.2] [sgdfc:6.2:0:8.7:0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4107	6720900_f2_1	5846	19949	522	174	YGI.095C	240	1.7(10)-19	Saccharomyces cerevisiae	[ui:yg 095c] [pn:vacuolar protein sorting-associated protein vps45] [gn:vps45:stt10] [gtcf:10.7:1.1:1:12.13:12.8] [keggfc:14.2] [sgdfc:3.2:0:6.2:0:8.5:0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG3468	4084567_f2_2	5847	19950	246	82	YHR110W	121	1.3(10)-7	Saccharomyces cerevisiae	[ui:yhr110w] [pn:similarity to human gp2512 protein:hyprothetical 24.2 kd protein in cdc12-orc6 intergenic region precursor] [gtcf:10.7:1.1:1] [keggfc:14.2] [sgdfc:6.2:0] [db:gtc-saccharomyces cerevisiae]

CONTIG3468	25788438_f1_1	5848	19951	435	145	YHR110W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:yhr110w] [pn:similarity to human gp2512 protein:hyprothetical 24.2 kd protein in cdc12-orc6 intergenic region precursor] [gicfc:10.7:1.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5445	4863437_c3_15	5849	19952	186	62	YIL173W	95	0.0022	Saccharomyces cerevisiae	[ui:yil173w] [pn:strong similarity to pep1p:putative membrane glycoprotein in suc2 5' region precursor] [gicfc:10.7:1.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5445	11929700_c1_7	5850	19953	858	286	YIL173W	154	6.0(10)-8	Saccharomyces cerevisiae	[ui:yil173w] [pn:strong similarity to pep1p:putative membrane glycoprotein in suc2 5' region precursor] [gicfc:10.7:1.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5445	2926675_c1_5	5851	19954	759	253	YIL173W	154	3.7(10)-8	Saccharomyces cerevisiae	[ui:yil173w] [pn:strong similarity to pep1p:putative membrane glycoprotein in suc2 5' region precursor] [gicfc:10.7:1.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1678	195442_f1_1	5852	19955	804	268	YIL154C	122	0.00013	Saccharomyces cerevisiae	[ui:yil154c] [pn:protein-sorting protein, vacuolar;vacuolar protein sorting-associated protein vps35] [gn:vps35:j0580] [gicfc:10.7:1.1:12.16] [keggfc:14.2] [sgdfe:6.2.0:9.10.0] [db:gic-saccharomyces cerevisiae]

CONTIG4984	25391251_c1_8	5853	19956	780	260	YJL154C	388	3.2(10)-51	Saccharomyces cerevisiae	[ui:yjl154c] [pn:protein-sorting protein, vacuolar:vacuolar protein sorting-associated protein vps35] [gn:vps35:j0580] [gtcf:10.7:1.1:12.16] [kegfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5545	4016642_f3_11	5854	19957	1053	351	YJL053W	655	2.2(10)-64	Saccharomyces cerevisiae	[ui:yjl053w] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1] [gn:pep8:j1152] [gtcf:10.7:1.1:12.16] [kegfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5218	4140825_f2_6	5855	19958	633	211	YKL196C	794	4.2(10)-79	Saccharomyces cerevisiae	[ui:ykl196c] [pn:similarity to sec22p:hyposhethal 22.7 kd protein in past-msl intergenic region] [gtcf:10.7:1.1:12.10:12.16] [kegfc:14.2] [sgdfc:6.2.0:8.3.0:9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5301	4884442_f1_2	5856	19959	930	310	YKL154W	179	1.3(10)-26	Saccharomyces cerevisiae	[ui:ykl154w] [pn:similarity to mouse signal recognition particle receptor beta subunit:putative signal recognition particle receptor beta subunit:sr-beta] [gn:ykl609] [gtcf:12.13:1.1.3] [kegfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5282	I382235_f2_2	5857	19960	1299	433	YKR001C	1437	3.2(10)-147	Saccharomyces cerevisiae	[ui:ykr001c] [pn:member of the dynamin family of gtpases:vacuolar sorting protein 1] [gn:vsp1:spo15:lam1] [gtcf:10.7:1.1:1.12.16] [kegfc:14.2] [sgdfc:6.2:0.9:4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5357	I0578562_c2_20	5858	19961	570	190	YKR001C	600	1.6(10)-58	Saccharomyces cerevisiae	[ui:ykr001c] [pn:member of the dynamin family of gtpases:vacuolar sorting protein 1] [gn:vsp1:spo15:lam1] [gtcf:10.7:1.1:1.12.16] [kegfc:14.2] [sgdfc:6.2:0.9:4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG463	20359635_f3_1	5859	19962	717	239	YKR014C	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:ykr014c] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt52] [gn:ypt52:yk112] [gtcf:10.7:1.1:1.12.13:12.6] [kegfc:14.2] [sgdfc:6.2:0.8:5.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5732	I5887_f3_22	5860	19963	615	205	YKR014C	307	1.7(10)-27	Saccharomyces cerevisiae	[ui:ykr014c] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt52] [gn:ypt52:yk112] [gtcf:10.7:1.1:1.12.13:12.6] [kegfc:14.2] [sgdfc:6.2:0.8:5.0:8.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2042	24398317_f1_1	5861	19964	486	162	YLR148W	224	2.0(10)-17	Saccharomyces cerevisiae	[ui:ylr148w] [pn:vacuolar membrane protein: vacuolar membrane protein pep3] [gn:pep3:vps18:19634] [gcfc:10.7:1.1:12.16] [kegfc:14.2] [sgdfc:6.2.0.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5010	23913202_f2_1	5862	19965	2436	812	YLR148W	346	5.0(10)-28	Saccharomyces cerevisiae	[ui:ylr148w] [pn:vacuolar membrane protein: vacuolar membrane protein pep3] [gn:pep3:vps18:19634] [gcfc:10.7:1.1:12.16] [kegfc:14.2] [sgdfc:6.2.0.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5505	6830381_c2_13	5863	19966	1983	661	YLR148W	270	2.0(10)-25	Saccharomyces cerevisiae	[ui:ylr148w] [pn:vacuolar membrane protein: vacuolar membrane protein pep3] [gn:pep3:vps18:19634] [gcfc:10.7:1.1:12.16] [kegfc:14.2] [sgdfc:6.2.0.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5291	4454500_f2_5	5864	19967	1125	375	YLR191W	478	3.0(10)-50	Saccharomyces cerevisiae	[ui:ylr191w] [pn:peroxisomal protein involved in protein import: peroxisomal membrane protein pas20: peroxin 13] [gn:pas20:pex13:19470] [gcfc:10.7:1.1:12.2:12.6] [kegfc:14.2] [sgdfc:6.2.0.8:4.0.9:8.0] [db:gtc-saccharomyces cerevisiae]



CONTIG5196	22304062_f1_1	5865	19968	291	97	YLR292C	106	5.0(10)-6	Saccharomyces cerevisiae	[ui:Ylr292c] [pn:er protein-translocation complex subunit:translocation protein sec72.p23] [gn:sec72:sec67:sim2.18003] [gtcf:10.7.1.1.12.16:12.6] [kegfc:14.2] [sgdfc:6.2.0.7.11.0:8.8.0.9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5432	1181442_f1_6	5866	19969	507	169	YLR378C	328	1.1(10)-29	Saccharomyces cerevisiae	[ui:Ylr378c] [pn:er protein-translocation complex subunit:protein transport protein sec61 alpha subunit] [gn:sec61.i3502] [gtcf:12.6.1.1.12.16:10.7] [kegfc:14.2] [sgdfc:6.2.0.7.11.0:8.8.0.9.4.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5450	644526_f3_6	5867	19970	975	325	YLR378C	1002	3.8(10)-101	Saccharomyces cerevisiae	[ui:Ylr378c] [pn:er protein-translocation complex subunit:protein transport protein sec61 alpha subunit] [gn:sec61.i3502] [gtcf:12.6.1.1.12.16:10.7] [kegfc:14.2] [sgdfc:6.2.0.7.11.0:8.8.0.9.4.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5669	953257_c2_25	5868	19971	2118	706	YLR396C	294	1.8(10)-24	Saccharomyces cerevisiae	[ui:ylr396c] [pn:vacuolar sorting protein:slp1 protein:vacuolar protein sorting protein 33] [gn:slp1:vps33:vam5:18084] [gicf:10.7:1.1:1.12.10:12.16] [kegfc:14.2] [sgdfc:6.2.0:8.3.0:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG2831	192137_f3_2	5869	19972	600	200	YML097C	247	1.3(10)-20	Saccharomyces cerevisiae	[ui:ym1097c] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps9] [gn:vps9:vpt9] [gicf:10.7:1.1:1.12.10:12.13] [kegfc:14.2] [sgdfc:6.2.0:8.3.0:8.5.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG2831	11728500_f2_1	5870	19973	1017	339	YML097C	312	1.2(10)-31	Saccharomyces cerevisiae	[ui:ym1097c] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps9] [gn:vps9:vpt9] [gicf:10.7:1.1:1.12.10:12.13] [kegfc:14.2] [sgdfc:6.2.0:8.3.0:8.5.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1858	25491258_f3_1	5871	19974	495	165	YMR004W	276	1.3(10)-23	Saccharomyces cerevisiae	[ui:ymr004w] [pn:required for vacuolar protein sorting:mvp1 protein] [gn:mvp1:ym8270] [gicf:10.7:1.1:1.12.13:12.16] [kegfc:14.2] [sgdfc:6.2.0:8.5.0:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG1858	25398561_f3_2	5872	19975	543	181	YMR004W	206	6.0(10)-16	Saccharomyces cerevisiae	[ui:ymr004w] [pn:required for vacuolar protein sorting:mvp1 protein] [gn:mvp1:ym8270] [gicf:10.7:1.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3364	819682_f1_1	5873	19976	1434	478	YMR091C	378	7.9(10)-50	Saccharomyces cerevisiae	[ui:ymr091c] [pn:nuclear protein localization factor:np16 protein] [gn:np16:ym9582] [gicf:10.7:1.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4357	25578887_c1_4	5874	19977	993	331	YMR214W	464	1.3(10)-55	Saccharomyces cerevisiae	[ui:ymr214w] [pn:similarity to to e.coli dhaj:scj1 protein] [gn:scj1:ym8261] [gicf:10.7:1.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG2466	4298260_f3_6	5875	19978	189	63	YNR006W	105	6.4(10)-5	Saccharomyces cerevisiae	[ui:ynr006w] [pn:vacuolar protein sorting-associated protein:vps27] [gn:vps27:grd11:n2038] [gicf:10.7:1.1:12.10:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.9.0] [db:gic-saccharomyces c

CONTIG346	2458276_f1_1	5876	19979	2241	747	YNR006W	358	1.3(10)-42	Saccharomyces cerevisiae	[ui:ym006w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps27] [gn:yps27:grd1:n2038] [gtcf:10.7.1.1:12.10:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.9.0] [db:gtc-saccharomyces c
CONTIG200	5906442_f3_2	5877	19980	468	156	YOL122C	238	3.1(10)-23	Saccharomyces cerevisiae	[ui:yol122c] [pn:manganese transporter:transporter protein smf/esp1] [gn:smf:esp1] [gtcf:12.6:10.7:1.1] [keggfc:14.2] [sgdfc:1.8.1:6.2.0:7.2.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1547	5344466_c3_4	5878	19981	654	218	YOL122C	422	1.1(10)-39	Saccharomyces cerevisiae	[ui:yol122c] [pn:manganese transporter:transporter protein smf/esp1] [gn:smf:esp1] [gtcf:12.6:10.7:1.1] [keggfc:14.2] [sgdfc:1.8.1:6.2.0:7.2.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2632	4103127_c1_5	5879	19982	1521	507	YOL122C	728	6.0(10)-118	Saccharomyces cerevisiae	[ui:yol122c] [pn:manganese transporter:transporter protein smf/esp1] [gn:smf:esp1] [gtcf:12.6:10.7:1.1] [keggfc:14.2] [sgdfc:1.8.1:6.2.0:7.2.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1162	1956388_f1_1	5880	19983	837	279	YOL062C	230	2.7(10)-36	Saccharomyces cerevisiae	[ui:yo1062c] [pn:clathrin-associate protein yap54] [gn:apm4] [gtcf:10.7:1.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2:0.8:3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5658	12898438_f1_1	5881	19984	369	123	YOL062C	255	2.5(10)-21	Saccharomyces cerevisiae	[ui:yo1062c] [pn:clathrin-associate protein yap54] [gn:apm4] [gtcf:10.7:1.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2:0.8:3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1497	23439632_c1_4	5882	19985	531	177	YOR016C	158	1.1(10)-11	Saccharomyces cerevisiae	[ui:yor016c] [pn:similarity to hamster cop-coated vesicle membrane protein] [gtcf:10.7:1.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1324	9852253_f3_3	5883	19986	444	148	YOR036W	127	7.2(10)-8	Saccharomyces cerevisiae	[ui:yor036w] [pn:syntaxin:t-snare:pep12 protein] [gn:pep12:vps6:vp13:or26] [gtcf:10.7:1.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2:0.8:5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5649	236258_c3_20	5884	19987	927	309	YOR036W	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:yor036w] [pn:syntaxin:t-snare:pep12 protein] [gn:pep12:vps6:vp13:or26] [gtcf:10.7:1.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2:0.8:5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

b2x18145.y	24862567_f3_1	5885	19988	471	157	YOR036W	142	1.5(10)-9	Saccharomyces cerevisiae	[ui:yor036w] [pn:syntaxin-t-snar:pep12 protein] [gn:pep12:vps6:vpl13:or26] [gctc:10.7:1.1:12.13:12.16] [kegfc:14.2] [sgdfc:6.2.0:8.5.0:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG2932	20081260_f1_1	5886	19989	714	238	YOR089C	723	1.3(10)-71	Saccharomyces cerevisiae	[ui:yor089c] [pn:gtp-binding protein:gtp-binding protein ypt51/vps21] [gn:ypt51:vps21:yor3154c] [gctc:10.7:1.1:12.10:12.13:12.16:12.6] [kegfc:14.2] [sgdfc:6.2.0:8.5.0:8.7.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG2891	22460877_c3_4	5887	19990	492	164	YOR132W	205	9.1(10)-16	Saccharomyces cerevisiae	[ui:yor132w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps17] [gn:vps17:pep21:c3314:yor3314w] [gctc:10.7:1.1] [kegfc:14.2] [sgdfc:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG707	25673905_f3_2	5888	19991	957	319	YOR132W	380	3.6(10)-39	Saccharomyces cerevisiae	[ui:yor132w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps17] [gn:vps17:pep21:c3314:yor3314w] [gctc:10.7:1.1] [kegfc:14.2] [sgdfc:6.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5413	4725328_c1_15	5889	19992	2031	677	YOR254C	1021	3.7(10)-103	Saccharomyces cerevisiae	[ui:yor254c] [pn:er protein-translocation complex subunit:np11 protein:sec63 protein] [gn:np11:sec63:pt11] [gtcf:10.7:11.1:12.16:12.6] [keggfc:14.2] [sgdfe:6.2:0.7.11.0:8.8:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4807	33260968_f2_5	5890	19993	285	95	YOR286W	221	2.2(10)-18	Saccharomyces cerevisiae	[ui:yor286w] [pn:similarity to d.melanogaster heat shock protein 67b2] [gtcf:12.7:11.1] [keggfc:14.2] [sgdfe:6.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1534	25597186_c2_4	5891	19994	228	76	YOR327C	288	1.8(10)-25	Saccharomyces cerevisiae	[ui:yor327c] [pn:strong similarity to synaptobrevin:synaptobrevin homolog 2] [gn:smc2] [gtcf:10.7:11.1:12.10:12.16] [keggfc:14.2] [sgdfe:6.2:0.8:3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG3832	19540675_f2_3	5892	19995	1422	474	YOR329C	203	3.7(10)-18	Saccharomyces cerevisiae	[ui:yor329c] [pn:suppressor of clathrin deficiency:scd5 protein:thb1 protein] [gn:scd5:thb1] [gtcf:10.7:11.1:12.6] [keggfc:14.2] [sgdfe:6.2:0.8:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5798	23875200_f1_9	5893	19996	627	209	YPL259C	588	2.8(10)-57	Saccharomyces cerevisiae	[ui:ypl259c] [pn:clathrin-associated protein:clathrin coat assembly protein ap54:clathrin coat associated protein ap54:golgi adaptor ap-1 54 kd protein:hal 54 kd subunit:clathrin assembly protein complex 1 medium chain] [gn:apm1:yap54:

CONTIG4518	22344008_f2_2	5894	19997	1131	377	YPL243W	134	7.2(10)-6	Saccharomyces cerevisiae	[ui:yp1243w] [pn:signal recognition particle protein:signal recognition particle 68 kd protein homolog] [gn:sp68] [gtcf:12.13:11.3] [kegfc:14.2] [sgdfc:6.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3924	11805416_f1_1	5895	19998	1353	451	YPL210C	114	1.3(10)-7	Saccharomyces cerevisiae	[ui:yp1210c] [pn:signal recognition particle protein:signal recognition particle 72 kd protein homolog] [gn:srp72] [gtcf:12.13:11.3] [kegfc:14.2] [sgdfc:6.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4942	22850187_c2_20	5896	19999	960	320	YPL094C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:yp1094c] [pn:er protein-translocation complex subunit:translocation protein sec62] [gn:sec62:lp614c] [gtcf:10.7:11.1:12.16:12.6] [kegfc:14.2] [sgdfc:6.2.0.7.11.0.8.8.0.9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3632	16882330_c3_9	5897	20000	975	325	YPL045W	201	2.3(10)-13	Saccharomyces cerevisiae	[ui:yp1045w] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps16] [gn:vps16:vam9] [gtcf:10.7:11.1:12.13:12.16] [kegfc:14.2] [sgdfc:6.2.0.8.5.0.9.3.0.9.10.0] [db:gtc-saccharomyces cerevisiae]



CONTIG3717	820337_c3_9	5898	20001	837	279	YPL045W	256	7.4(10)-28	Saccharomyces cerevisiae	[ui:yp1045w] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps16] [gn:vps16:yam9] [gcf:10.7:1.1:1.2.13:12.16] [kegfc:14.2] [sgdfc:6.2:0:8.5:0:9.3:0:9.10:0] [db:gic-saccharomyces cerevisiae]
CONTIG3717	10650305_c1_6	5899	20002	543	181	YPL045W	113	0.00033	Saccharomyces cerevisiae	[ui:yp1045w] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps16] [gn:vps16:yam9] [gcf:10.7:1.1:1.2.13:12.16] [kegfc:14.2] [sgdfc:6.2:0:8.5:0:9.3:0:9.10:0] [db:gic-saccharomyces cerevisiae]
CONTIG2805	9860458_f3_4	5900	20003	759	253	YPR088C	372	2.3(10)-34	Saccharomyces cerevisiae	[ui:yp1088c] [pn:signal recognition particle subunit:signal recognition particle 54 kd protein homolog:srp54] [gn:srp54:sth1:p9513] [gcf:12.13:1.1:3] [kegfc:14.2] [sgdfc:6.2:0:9.2:0] [db:gic-saccharomyces cerevisiae]
CONTIG1222	4954650_c1_4	5901	20004	888	296	YCR077C	98	0.019	Saccharomyces cerevisiae	[ui:ycr077c] [pn:topoisomerase ii-associated protein:88.5 kd protein in ers1-srb8 intergenic region] [gcf:10.8] [kegfc:14.2] [sgdfc:3.6:0:3.7:0:9.2:0] [db:gic-saccharomyces cerevisiae]

CONTIG1542	787811_c3_7	5902	20005	762	254	YCR077C	415	4.4(10)-38	Saccharomyces cerevisiae	[ui:ycr077c] [pn:topoisomerase ii-associated protein:88.5 kd protein in ers1-srb8 intergenic region] [gctfc:10.8] [keggfc:14.2] [sgdfe:3.6:0:3.7:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5531	4179691_c2_33	5903	20006	1692	564	YDR206W	134	9.8(10)-10	Saccharomyces cerevisiae	[ui:ydr206w] [pn:similarity to est1 protein] [gctfc:10.8] [keggfc:14.2] [sgdfe:3.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4719	36210197_c2_4	5904	20007	1488	496	YGI201C	1446	2.2(10)-174	Saccharomyces cerevisiae	[ui:ygi201c] [pn:similarity with rat intestinal dna replication protein:hypothetical 113.0 kd protein in kex1-emp24 intergenic region] [gctfc:10.8] [keggfc:14.2] [sgdfe:3.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5624	10975253_c3_19	5905	20008	1059	353	YGI201C	662	1.8(10)-94	Saccharomyces cerevisiae	[ui:ygi201c] [pn:similarity with rat intestinal dna replication protein:hypothetical 113.0 kd protein in kex1-emp24 intergenic region] [gctfc:10.8] [keggfc:14.2] [sgdfe:3.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5612	10973406_f3_7	5906	20009	858	286	YGR132C	979	1.1(10)-98	Saccharomyces cerevisiae	[ui:ygr132c] [pn:prohibitin, antiproliferative protein:prohibitin] [gn:phb1:phb] [gctfc:10.8:12.8] [keggfc:14.2] [sgdfe:3.6:0:3.8:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4991	20601678_c2_5	5907	20010	975	325	YGR231C	1010	5.5(10)-102	Saccharomyces cerevisiae	[ui:yg231c] [pn:strong similarity to prohibits:hypothetical 34.9 kd protein in smi1-pho81 intergenic region] [gn:g8561] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfc:3.6:0.3:8.0] [db:gic-saccharomyces cerevisiae]
CONTIG2191	24336567_c3_5	5908	20011	1299	433	YIL150C	290	1.2(10)-23	Saccharomyces cerevisiae	[ui:yil150c] [pn:required for s-phase initiation or completion:protein] [gn:dna43] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfc:3.6:0.3:8.0] [db:gic-saccharomyces cerevisiae]
CONTIG4281	36597763_f3_2	5909	20012	258	86	YKL113C	128	1.0(10)-7	Saccharomyces cerevisiae	[ui:ykl113c] [pn:ssdna endonuclease and 5'-3'exonuclease:structure specific endonuclease ykl113c/] [gn:rad27.ykl1510] [gtcf:10.8] [kegfc:14.2] [sgdfc:3.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG4404	14477175_c1_7	5910	20013	675	225	YKL113C	671	4.7(10)-66	Saccharomyces cerevisiae	[ui:ykl113c] [pn:ssdna endonuclease and 5'-3'exonuclease:structure specific endonuclease ykl113c/] [gn:rad27.ykl1510] [gtcf:10.8] [kegfc:14.2] [sgdfc:3.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG5535	39125_f2_5	5911	20014	1803	601	YLR103C	310	6.2(10)-67	Saccharomyces cerevisiae	[ui:ylr103c] [pn:required for minichromosome maintenance and initiation of chromosomal dna replication] [gn:cdc45] [gtcf:10.8:12.8] [kegfc:13.2] [sgdfc:3.6:0.3:8.0] [db:gic-saccharomyces cerevisiae]

CONTIG5343	6251_f2_4	5912	20015	1962	654	YOL095C	278	5.2(10)-32	Saccharomyces cerevisiae	[ui:yo1095c] [pn:similarity to s.aureus dna helicase pcal] [gtcf:10.8] [kegfc:14.2]
										[sgdfe:3.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG2784	11751500_f3_3	5913	20016	1536	512	YPL256C	336	3.8(10)-30	Saccharomyces cerevisiae	[ui:yp1256c] [pn:cyclin, g1/s-specific:g1/s-specific cyclin] [gn:cln2] [gtcf:10.8:12.8:12.9] [kegfc:13.1] [sgdfe:3.2.0:3.3.0:3.6.0:3.8.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1980	4413900_f3_3	5914	20017	684	228	YPR019W	271	1.8(10)-22	Saccharomyces cerevisiae	[ui:yp1019w] [pn:member of the cdc46p/mcm2p/mcm3p family:cell division control protein 54] [gn:cdc54:hcd21:yp9531] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfe:3.6.0:3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG474	7159683_c3_3	5915	20018	492	164	YPR019W	359	7.2(10)-32	Saccharomyces cerevisiae	[ui:yp1019w] [pn:member of the cdc46p/mcm2p/mcm3p family:cell division control protein 54] [gn:cdc54:hcd21:yp9531] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfe:3.6.0:3.8.0] [db:gic-saccharomyces cerevisiae]
b9x12m21.y	236094_cl_1	5916	20019	519	173	YPR019W	593	3.2(10)-57	Saccharomyces cerevisiae	[ui:yp1019w] [pn:member of the cdc46p/mcm2p/mcm3p family:cell division control protein 54] [gn:cdc54:hcd21:yp9531] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfe:3.6.0:3.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG4270	10413432_c2_5	5917	20020	1497	499	YPR120C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ypri20c] [pn:cyclin, b-type:spase entry cyclin 5] [gn:cb5:p9642] [gctc:10.8:12.8] [kegfc:1.3.3] [sgdfc:3.6:0.3:8.0] [db:gic-saccharomyces cerevisiae]
CONTIG2912	36224063_f2_2	5918	20021	1308	436	YBR136W	780	5.2(10)-76	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gctc:10.8:12.8] [kegfc:14.2] [sgdfc:3.5:0.3:7.0:3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3833	1986000_c2_11	5919	20022	345	115	YBR136W	154	1.8(10)-9	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gctc:10.8:12.8] [kegfc:14.2] [sgdfc:3.5:0.3:7.0:3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3833	35212787_c2_10	5920	20023	1440	480	YBR136W	526	5.4(10)-49	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gctc:10.8:12.8] [kegfc:14.2] [sgdfc:3.5:0.3:7.0:3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3833	14195175_c3_12	5921	20024	966	322	YBR136W	302	3.5(10)-25	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gctc:10.8:12.8] [kegfc:14.2] [sgdfc:3.5:0.3:7.0:3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG4697	30515925_f2_1	5922	20025	2334	778	YBR136W	122	0.0027	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gctc:10.8:12.8] [kegfc:14.2] [sgdfc:3.5:0.3:7.0:3.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG4748	10647936_c3_12	5923	20026	690	230	YDL059C	184	1.8(10)-14	Saccharomyces cerevisiae	[ui:ydl059c] [pn:recombination and dna repair protein] [gn:rad59] [gtcf:10.8] [kegfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5676	1178882_c2_22	5924	20027	1284	428	YDR182W	872	2.3(10)-87	Saccharomyces cerevisiae	[ui:ydr182w] [pn:cell division control protein] [gn:cdc1:esp2:y09395] [gtcf:10.8:12.15:12.8] [kegfc:14.2] [sgdfc:3.2.0:3.4.0:3.7.0:3.8.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5727	4079660_f1_3	5925	20028	1467	489	YDR182W	552	1.8(10)-53	Saccharomyces cerevisiae	[ui:ydr182w] [pn:cell division control protein:cell division control protein 1] [gn:cdc1:dsr1:esp2:y09395] [gtcf:10.8:12.15:12.8] [kegfc:14.2] [sgdfc:3.2.0:3.4.0:3.7.0:3.8.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5715	6910183_f1_1	5926	20029	660	220	YER173W	244	2.6(10)-25	Saccharomyces cerevisiae	[ui:yer173w] [pn:cell cycle checkpoint protein:checkpoint protein rad24] [gn:rad24:sgp-orf60] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5715	5312513_f2_4	5927	20030	978	326	YER173W	119	3.6(10)-7	Saccharomyces cerevisiae	[ui:yer173w] [pn:cell cycle checkpoint protein:checkpoint protein rad24] [gn:rad24:sgp-orf60] [gtcf:10.8:12.8] [kegfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5553	976556_c2_22	5928	20031	1530	510	YHR031C	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:yhr031c] [pn:similarity to pit1p:hypothetical helicase in slt2-put2 intergenic region] [gtcf:10.8] [kegfc:14.2] [sgdfc:3.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5801	21657817_f2_9	5929	20032	2739	913	YHR031C	743	9.0(10)-96	Saccharomyces cerevisiae	[ui:yhr031c] [pn:similarity to pit1p:hypothetical helicase in slt2-put2 intergenic region] [gtcf:10.8] [kegfc:14.2] [sgdfc:3.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5553	23829836_c1_18	5930	20033	303	101	YHR031C	221	2.8(10)-17	Saccharomyces cerevisiae	[ui:yhr031c] [pn:similarity to pit1p:hypothetical helicase in slt2-put2 intergenic region] [gtcf:10.8] [kegfc:14.2] [sgdfc:3.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4667	23611251_c3_11	5931	20034	342	114	YHR154W	154	7.4(10)-10	Saccharomyces cerevisiae	[ui:yhr154w] [pn:putative dna damage responsive cell cycle checkpoint protein: hypothetical 123.0 kd protein in spo16-rec104 intergenic region] [gtcf:10.8-12.8] [kegfc:14.2] [sgdfc:3.7.0.3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG4709	14729561_c1_13	5932	20035	807	269	YHR154W	97	0.11	Saccharomyces cerevisiae	[ui:yhr154w] [pn:putative dna damage responsive cell cycle checkpoint protein: hypothetical 123.0 kd protein in spo16-rec104 intergenic region] [gtcf:10.8-12.8] [kegfc:14.2] [sgdfc:3.7.0.3.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG5190	14554813_f3_5	5933	20036	1629	543	YHR154W	350	5.0(10)-29	Saccharomyces cerevisiae	[ui:Yhr154w] [pn:putative dna damage responsive cell cycle checkpoint protein: hypothetical 123.0 kd protein in spo16-rec104 intergenic region] [gtcf:10.8:12.8] [keggfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1194	15818812_f3_1	5934	20037	471	157	YLR383W	306	4.7(10)-26	Saccharomyces cerevisiae	[ui:Ylr383w] [pn:recombination repair protein] [gn:rhc18] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG232	16462551_c1_2	5935	20038	1227	409	YLR383W	218	8.5(10)-15	Saccharomyces cerevisiae	[ui:Ylr383w] [pn:recombination repair protein] [gn:rhc18] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG865	35370305_c2_6	5936	20039	921	307	YLR383W	328	2.1(10)-28	Saccharomyces cerevisiae	[ui:Ylr383w] [pn:recombination repair protein] [gn:rhc18] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	26354683_f2_12	5937	20040	2640	880	YMR190C	1739	3.0(10)-183	Saccharomyces cerevisiae	[ui:Ymr190c] [pn:dna helicase:hellicase sgs1] [gn:sgs1:tpsl:ym9646] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5430	20426588_f3_8	5938	20041	825	275	YOR077W	347	1.0(10)-31	Saccharomyces cerevisiae	[ui:Yor077w] [pn:similarity to mouse kin17 protein:protein] [gn:mts2] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]



CONTIG5699	24275806_c1_21	5939	20042	993	331	YPL164C	291	8.3(10)-25	Saccharomyces cerevisiae	[ui:yp1164c] [pn:similarity to mismatch repair protein mlh1 p] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1704	12694430_f2_2	5940	20043	606	202	YPL164C	197	1.1(10)-14	Saccharomyces cerevisiae	[ui:yp1164c] [pn:similarity to mismatch repair protein mlh1 p] [gtcf:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5807	9972786_f3_5	5941	20044	528	176	YPL121C	151	5.9(10)-11	Saccharomyces cerevisiae	[ui:yp1121c] [pn:meiotic protein:meiosis protein 5] [gn:mei5] [gtcf:10.8.12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5650	265902_c3_23	5942	20045	1449	483	YBR236C	612	8.4(10)-60	Saccharomyces cerevisiae	[ui:ybr236c] [pn:methyltransferase:abd1 protein] [gn:abd1:ybr1602] [gtcf:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4457	4331510_c2_9	5943	20046	543	181	YJR017C	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:yjr017c] [pn:essl protein:processing/termination factor 1] [gn:essl:ptf1:j1452] [gtcf:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2527	11179687_c1_6	5944	20047	1617	539	YKL025C	404	9.4(10)-47	Saccharomyces cerevisiae	[ui:ykl025c] [pn:component of the pab1p-dependent poly:a ribonuclease:hypothetical 76.5 kd protein in tfa1-ura6 intergenic region] [gn:pan3] [gtcf:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3251	21682687_c2_5	5945	20048	414	138	YLR115W	143	8.3(10)-9	Saccharomyces cerevisiae	[ui:yr115w] [pn:similarity to cattle cleavage and polyadenylation specificity factor] [gcf:10.9] [kegfc:14.2] [sgdfc:4.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG4585	14648437_c3_12	5946	20049	1038	346	YLR115W	495	1.2(10)-46	Saccharomyces cerevisiae	[ui:yr115w] [pn:similarity to cattle cleavage and polyadenylation specificity factor] [gcf:10.9] [kegfc:14.2] [sgdfc:4.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG3608	14640686_f2_3	5947	20050	579	193	YOL149W	168	6.5(10)-26	Saccharomyces cerevisiae	[ui:yol149w] [pn:component of the yeast decapping enzyme] [gn:dop1] [gcf:10.9] [kegfc:14.2] [sgdfc:4.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG5771	24414192_f3_18	5948	20051	426	142	YPL178W	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:yp1178w] [pn:cell cycle block in meiotic prophase] [gn:sae1] [gcf:10.9:12.8] [kegfc:14.2] [sgdfc:3.8.0:4.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG5785	14511013_c3_35	5949	20052	696	232	YAL059W	109	2.8(10)-5	Saccharomyces cerevisiae	[ui:yal059w] [pn:involved in cell wall biosynthesis:protein] [gn:sim1] [gcf:1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG2940	21600465_f2_4	5950	20053	306	102	YBR068C	143	5.2(10)-9	Saccharomyces cerevisiae	[ui:ybr068c] [pn:amino acid permease:leu/val/ile amino-acid permease bap2] [gn:bap2:ybr0629] [gicf:1.1.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG4339	20593915_f1_1	5951	20054	1020	340	YBR298C	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:ybr298c] [pn:maltose permease] [gn:mal3i:mal3i:mal6i:mal6i:ybr2116] [gicf:1.1.1:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3:0.8:7.0:9.1:0] [db:gic-saccharomyces cerevisiae]
CONTIG2329	448958_f2_1	5952	20055	606	202	YCL027W	122	2.0(10)-5	Saccharomyces cerevisiae	[ui:ycl027w] [pn:cell fusion protein:nuclear fusion protein fus1] [gn:fus1:ycl27w] [gicf:1.1.1:12.8:12.9] [keggfc:14.2] [sgdfc:3.0:9.1:0:10.1:6] [db:gic-saccharomyces cerevisiae]
CONTIG1755	34117012_c3_5	5953	20056	393	131	YCR011C	292	1.3(10)-24	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease:probable atp-dependent permease precursor] [gn:adp1:ycr11c:ycr105] [gicf:1.1.1:12.6] [keggfc:14.2] [sgdfc:7.0:9.1:0] [db:gic-saccharomyces cerevisiae]

CONTIG1755	21687875_c1_3	5954	20057	861	287	YCR011C	676	5.5(10)-66	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease:probable atp-dependent permease precursor] [gn:adp1:ycr11c:ycr1051] [gctc:1.1:1.12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2857	4394530_c3_5	5955	20058	1008	336	YCR011C	957	2.2(10)-96	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease:probable atp-dependent permease precursor] [gn:adp1:ycr11c:ycr1051] [gctc:1.1:1.12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3284	1408501_f3_2	5956	20059	465	155	YCR011C	238	7.7(10)-19	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease:probable atp-dependent permease precursor] [gn:adp1:ycr11c:ycr1051] [gctc:1.1:1.12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5055	32305143_c2_11	5957	20060	4089	1363	YCR038C	305	2.7(10)-31	Saccharomyces cerevisiae	[ui:ycr038c] [pn:gdp/gtp exchange factor for rsr1p/bud1p:bud site selection protein bud5] [gn:bud5:ycr38c:ycr526] [gctc:1.1:1.12.8] [kegfc:13.3] [sgdfe:3.2.0:9.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG1269	14472817_fl_1	5958	20061	984	328	YCR098C	385	9.5(10)-36	Saccharomyces cerevisiae	[ui:yer098c] [pn:similarity to phosphate transporter proteins;probable metabolic transport protein yer98c] [gn:git1:yer98c:yer137] [gtcf:12.4:1.1:13.10] [kegfc:14.2] [sgdfe:1.4.3:7.2.3:7.3.0.9.1.0:17.0.0] [db:gtc-saccharomyces cer]
CONTIG4599	484681_c3_9	5959	20062	999	333	YCR098C	297	6.9(10)-26	Saccharomyces cerevisiae	[ui:yer098c] [pn:similarity to phosphate transporter proteins;probable metabolic transport protein yer98c] [gn:git1:yer98c:yer137] [gtcf:12.4:1.1:13.10] [kegfc:14.2] [sgdfe:1.4.3:7.2.3:7.3.0.9.1.0:17.0.0] [db:gtc-saccharomyces cer]
CONTIG4599	5913317_c3_8	5960	20063	468	156	YCR098C	174	1.8(10)-12	Saccharomyces cerevisiae	[ui:yer098c] [pn:similarity to phosphate transporter proteins;probable metabolic transport protein yer98c] [gn:git1:yer98c:yer137] [gtcf:12.4:1.1:13.10] [kegfc:14.2] [sgdfe:1.4.3:7.2.3:7.3.0.9.1.0:17.0.0] [db:gtc-saccharomyces cer]

CONTIG4947	4334552_f1_1	5961	20064	930	310	YCR098C	921	1.5(10)-92	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolic transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcf:12.4:1.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2.3:7.3.0:9.1.0:17.0.0] [db:gic-saccharomyces cer
CONTIG98	20959800_c1_1	5962	20065	594	198	YCR098C	224	7.0(10)-18	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolic transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcf:12.4:1.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2.3:7.3.0:9.1.0:17.0.0] [db:gic-saccharomyces cer
CONTIG3589	14235307_f2_1	5963	20066	1599	533	YDL210W	1196	1.1(10)-121	Saccharomyces cerevisiae	[ui:ydl210w] [pn:gaba-specific high-affinity permease:gaba-specific permease:gaba-specific transport protein] [gn:uga4:d1037] [gtcf:11.1:12.1] [keggfc:14.2] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5100	11844785_f3_1	5964	20067	1428	476	YDL210W	1063	1.3(10)-107	Saccharomyces cerevisiae	[ui:ydl210w] [pn:gaba-specific high-affinity permease:gaba-specific permease:gaba-specific transport protein] [gn:uga4:d1037] [gtcf:11.1:12.1] [keggfc:14.2] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5563	20969078_f2_6	5965	20068	2298	766	YDL194W	1369	5.0(10)-140	Saccharomyces cerevisiae	[ui:ydl194w] [pn:high-affinity glucose transporter/regulatory protein:high-affinity glucose transporter snf3] [gn:snf3:d1234] [gtcf:12.2:1.1:12.13] [kegfc:14.2] [sgdfe:1.5.2:1.5.3:7.3:0.8:7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cer
b4x10274.y	9860017_f1_1	5966	20069	405	135	YDL194W	135	6.2(10)-8	Saccharomyces cerevisiae	[ui:ydl194w] [pn:high-affinity glucose transporter/regulatory protein:high-affinity glucose transporter snf3] [gn:snf3:d1234] [gtcf:12.2:1.1:12.13] [kegfc:14.2] [sgdfe:1.5.2:1.5.3:7.3:0.8:7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cer
CONTIG1940	26172692_c1_2	5967	20070	1077	359	YDR011W	1022	1.0(10)-102	Saccharomyces cerevisiae	[ui:ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:yd8119] [gtcf:11.1:12.12:12.6] [kegfc:14.2] [sgdfe:7.9:0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG665	23838938_c3_4	5968	20071	915	305	YDR011W	535	2.7(10)-50	Saccharomyces cerevisiae	[ui:ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:yd8119] [gtcf:11.1:12.12:12.6] [kegfc:14.2] [sgdfe:7.9:0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG900	5269432_f3_1	5969	20072	801	267	YDR011W	244	2.8(10)-19	Saccharomyces cerevisiae	[ui:Ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:Ydr8119] [gfc:1.1:1.12.12:12.6] [kegfc:14.2] [sgdfe:7.9.0.9.1.0:1.1.3.0] [db:gtc-saccharomyces cerevisiae]
b1x17948.x	21611632_c1_1	5970	20073	831	277	YDR011W	618	3.8(10)-59	Saccharomyces cerevisiae	[ui:Ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:Ydr8119] [gfc:1.1:1.12.12:12.6] [kegfc:14.2] [sgdfe:7.9.0.9.1.0:1.1.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4946	26354552_c2_7	5971	20074	339	113	YDR342C	108	2.7(10)-5	Saccharomyces cerevisiae	[ui:Ydr342c] [pn:high-affinity hexose transporter:hxt6] [gn:hxt7:d9651] [gfc:12.2:1.1.1] [kegfc:14.2] [sgdfe:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5043	814092_c2_10	5972	20075	1521	507	YDR342C	1320	7.9(10)-135	Saccharomyces cerevisiae	[ui:Ydr342c] [pn:high-affinity hexose transporter:hxt6] [gn:hxt7:d9651] [gfc:12.2:1.1.1] [kegfc:14.2] [sgdfe:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]



CONTIG5004	5866544_c1_2	5973	20076	1257	419	YDR342C	1100	1.6(10)-111	Saccharomyces cerevisiae	[ui:ydr342c] [pn:high-affinity hexose transporter:hxt6] [gn:hxt7:d9651] [gctfc:12.2:1.1] [keggfc:14.2] [sgdfe:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG473	25423837_f1_1	5974	20077	648	216	YDR497C	256	3.1(10)-21	Saccharomyces cerevisiae	[ui:ydr497c] [pn:myo-inositol permease, major myo-inositol transporter 1] [gn:itrl:d9719] [gctfc:12.2:1.1.8.2] [keggfc:14.2] [sgdfe:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5237	4069677_f1_2	5975	20078	1662	554	YDR536W	1639	1.2(10)-168	Saccharomyces cerevisiae	[ui:ydr536w] [pn:strong similarity to members of the sugar permease family:sugar transporter stl1] [gn:stl1:d9719] [gctfc:12.2:1.1] [keggfc:14.2] [sgdfe:1.5.3:7.3.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5348	26360285_f1_3	5976	20079	1503	501	YDR536W	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:ydr536w] [pn:strong similarity to members of the sugar permease family:sugar transporter stl1] [gn:stl1:d9719] [gctfc:12.2:1.1] [keggfc:14.2] [sgdfe:1.5.3:7.3.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3348	13712753_f3_10	5977	20080	273	91	YDR536W	150	8.3(10)-10	Saccharomyces cerevisiae	[ui:ydr536w] [pn:strong similarity to members of the sugar permease family:sugar transporter stil] [gn:stl:d9719] [gtcf:12.2:1.1] [kegfc:14.2] [sgdf:1.5.3:7.3:0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3655	32455327_c3_22	5978	20081	978	326	YEL069C	289	7.2(10)-25	Saccharomyces cerevisiae	[ui:yel069c] [pn:high-affinity hexose transporter:hexose transporter hxt13] [gn:hxt13:hxt8] [gtcf:12.2:1.1] [kegfc:14.2] [sgdf:1.5.3:7.3:0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2731	19532625_c1_3	5979	20082	1317	439	YEL063C	1315	2.7(10)-134	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcf:11.1:12.1:12.6] [kegfc:14.2] [sgdf:1.1.3:7.4:0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3177	2914055_c2_3	5980	20083	432	144	YEL063C	232	1.3(10)-18	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcf:11.1:12.1:12.6] [kegfc:14.2] [sgdf:1.1.3:7.4:0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3579	10033577_c2_6	5981	20084	798	266	YEL063C	709	4.4(10)-70	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcf:11.1:12.1:12.6] [kegfc:14.2] [sgdf:1.1.3:7.4:0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4383	2397692_f1_1	5982	20085	594	198	YEL063C	540	3.6(10)-52	Saccharomyces cerevisiae	[ui:yeI063c] [pn:amino acid permease:arginine permease] [gn:can1] [gfcf:1.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1:3:7.4:0.8:7.0:9.1:0:17.0.0] [db:gfc-saccharomyces cerevisiae]
CONTIG4559	36564036_f2_1	5983	20086	1215	405	YEL063C	1160	7.0(10)-118	Saccharomyces cerevisiae	[ui:yeI063c] [pn:amino acid permease:arginine permease] [gn:can1] [gfcf:1.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1:3:7.4:0.8:7.0:9.1:0:17.0.0] [db:gfc-saccharomyces cerevisiae]
CONTIG96	13719753_c2_1	5984	20087	618	206	YEL063C	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:yeI063c] [pn:amino acid permease:arginine permease] [gn:can1] [gfcf:1.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1:3:7.4:0.8:7.0:9.1:0:17.0.0] [db:gfc-saccharomyces cerevisiae]
CONTIG2651	15126675_c1_6	5985	20088	1221	407	YER056C	1172	3.7(10)-119	Saccharomyces cerevisiae	[ui:yer056c] [pn:purine-cytosine permease:pcp:cytosine/purine transport protein] [gn:fcy2] [gfcf:12.3:1.1:4.1:4.2] [keggfc:14.2] [sgdfc:1.3:7.7:6.0:8.7:0:9.1:0:17.0.0] [db:gfc-saccharomyces cerevisiae]

CONTIG105	35267137_c2_2	5986	20089	444	148	YER118C	199	1.3(10)-15	Saccharomyces cerevisiae	[ui:yer118c] [pn:involved in the hog1 high-osmolarity signal transduction pathway:ssu81 protein:ssu81 osmosensor] [gn:ssu81:sho1] [gtcf:12.13:11.3] [keggfc:14.2] [sgdfc:9.1.0:10.3.3:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4313	160902_f1_3	5987	20090	1155	385	YER118C	270	1.3(10)-27	Saccharomyces cerevisiae	[ui:yer118c] [pn:involved in the hog1 high-osmolarity signal transduction pathway:ssu81 protein:ssu81 osmosensor] [gn:ssu81:sho1] [gtcf:12.13:11.3] [keggfc:14.2] [sgdfc:9.1.0:10.3.3:11.1.0] [db:gtc-saccharomyces cerevisiae]
b9x10g01.y	1032761_c1_2	5988	20091	573	191	YFL026W	201	1.3(10)-15	Saccharomyces cerevisiae	[ui:yfl026w] [pn:pheromone alpha-factor receptor:pheromone alpha factor receptor] [gn:ste2] [gtcf:11.1:11.3:12.8:12.9] [keggfc:13.1] [sgdfc:3.0:9.1.0:10.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	35189635_c2_52	5989	20092	1224	408	YFL011W	331	1.5(10)-29	Saccharomyces cerevisiae	[ui:yfl011w] [pn:hexose transporter] [gn:hxt10] [gtcf:12.2:11.1] [keggfc:14.2] [sgdfc:1.5:3.7:3.0:8.7:0.9:1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4079	23939651_c1_4	5990	20093	1872	624	YGL233W	282	2.6(10)-21	Saccharomyces cerevisiae	[ui:ygl233w] [pn:vesicular traffic control protein] [gn:sec15] [gtcf:11.1:12.10] [keggfc:14.2] [sgdfc:8.3.0:8.6:0.9:1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4714	12897316_f2_1	5991	20094	678	226	YGL233W	113	2.7(10)-10	Saccharomyces cerevisiae	[ui:yg1233w] [pn:vesicular traffic control protein] [gn:sec15] [gctc:1.1:12.10] [keggfc:14.2] [sgdfe:8.3:0:8.0:9.1:0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3746	12188155_f2_2	5992	20095	1353	451	YGL077C	1117	2.6(10)-113	Saccharomyces cerevisiae	[ui:yg1077c] [pn:choline permease:choline transport protein] [gn:hnm1:ctr1:ctr] [gctc:12.2:11.1] [keggfc:14.2] [sgdfe:7.4:0:8.7:0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5418	26189005_c1_10	5993	20096	1758	586	YGL077C	1185	1.6(10)-120	Saccharomyces cerevisiae	[ui:yg1077c] [pn:choline permease:choline transport protein] [gn:hnm1:ctr1:ctr] [gctc:12.2:11.1] [keggfc:14.2] [sgdfe:7.4:0:8.7:0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG848	24882176_c2_6	5994	20097	1143	381	YGL077C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:yg1077c] [pn:choline permease:choline transport protein] [gn:hnm1:ctr1:ctr] [gctc:12.2:11.1] [keggfc:14.2] [sgdfe:7.4:0:8.7:0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3434	10725014_c1_7	5995	20098	1695	565	YGL008C	2253	1.1(10)-233	Saccharomyces cerevisiae	[ui:yg1008c] [pn:h+-transporting p-type atpase:plasma membrane atpase 1:proton pump] [gn:pma1] [gctc:12.5:1.1] [ec:3.6.1.35] [keggfc:14.1] [sgdfe:1.8:2:7.2:7.8:0:9.1:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4102	24397650_c2_3	5996	20099	1083	361	YGR009C	260	1.5(10)-21	Saccharomyces cerevisiae	[ui:Ygr009c] [pn:protein transport protein:protein transport protein sec9] [gn:sec9:hss7] [gtcf:12.6:1.1:12.10] [kegfc:14.2] [sgdfc:8.3:0.8:6.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG764	24509563_c2_1	5997	20100	192	64	YGR009C	147	2.1(10)-9	Saccharomyces cerevisiae	[ui:Ygr009c] [pn:protein transport protein:protein transport protein sec9] [gn:sec9:hss7] [gtcf:12.6:1.1:12.10] [kegfc:14.2] [sgdfc:8.3:0.8:6.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5663	4195250_c2_16	5998	20101	2403	801	YGR014W	94	0.76	Saccharomyces cerevisiae	[ui:Ygr014w] [pn:multicopy suppressor of a cdc24 bud emergence defect:protein:multicopy suppression of a budding defect 2] [gn:msb2] [gtcf:1.1:1:12.8] [kegfc:14.2] [sgdfc:3.2:0.9:1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3541	553336_c3_3	5999	20102	666	222	YGR055W	340	1.8(10)-30	Saccharomyces cerevisiae	[ui:Ygr055w] [pn:high affinity methionine permease] [gn:mup1] [gtcf:1.1:1:12.1:12.6] [kegfc:14.2] [sgdfc:1.1:3:7.4:0.8:7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2940	813803_f1_1	6000	20103	852	284	YGR191W	451	9.5(10)-43	Saccharomyces cerevisiae	[ui:Ygr191w] [pn:histidine permease] [gn:hip1:g7572] [gtcf:1.1:1:12.1:12.6] [kegfc:14.2] [sgdfc:1.1:3:7.4:0.8:7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG57	31533281_f3_2	6001	20104	630	210	YGR191W	497	1.3(10)-47	Saccharomyces cerevisiae	[ui: ygr191w] [pn: histidine permease] [gn: hipl.g/572] [gtcf: 1.1:1.12.6] [keggfc: 14.2] [sgdfc: 1.1.3:7.4.0.8:7.0.9:1.0:17.0.0] [db: gtc-saccharomyces cerevisiae]
CONTIG1342	3172050_c2_2	6002	20105	1086	362	YGR281W	464	5.5(10)-48	Saccharomyces cerevisiae	[ui: ygr281w] [pn: atp-binding cassette transporter protein: oligomycin resistance atp-dependent permease] [gn: yor1] [gtcf: 1.1:1.12.6:13.3] [keggfc: 14.2] [sgdfc: 7.9.0:7.10.0:9.1.0] [db: gtc-saccharomyces cerevisiae]
CONTIG1526	4469127_f2_2	6003	20106	462	154	YGR281W	234	3.2(10)-18	Saccharomyces cerevisiae	[ui: ygr281w] [pn: atp-binding cassette transporter protein: oligomycin resistance atp-dependent permease] [gn: yor1] [gtcf: 1.1:1.12.6:13.3] [keggfc: 14.2] [sgdfc: 7.9.0:7.10.0:9.1.0] [db: gtc-saccharomyces cerevisiae]
CONTIG1500	24901912_f1_1	6004	20107	723	241	YGR281W	512	9.6(10)-72	Saccharomyces cerevisiae	[ui: ygr281w] [pn: atp-binding cassette transporter protein: oligomycin resistance atp-dependent permease] [gn: yor1] [gtcf: 1.1:1.12.6:13.3] [keggfc: 14.2] [sgdfc: 7.9.0:7.10.0:9.1.0] [db: gtc-saccharomyces cerevisiae]

b2x10882.x	24891016_c3_2	6005	20108	495	165	YGR281W	182	1.1(10)-12	Saccharomyces cerevisiae	[ui:Ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance ap-dependent permease] [gn:yor1] [gdcf:11.1:12.6:13.3] [keggf:14.2] [sgdcf:7.9.0:7.10.0:9.1.0] [db:gic-saccharomyces cerevisiae]
b3x10485.y	4004139_c1_1	6006	20109	513	171	YGR281W	499	1.8(10)-46	Saccharomyces cerevisiae	[ui:Ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance ap-dependent permease] [gn:yor1] [gdcf:11.1:12.6:13.3] [keggf:14.2] [sgdcf:7.9.0:7.10.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3184	4884677_c3_9	6007	20110	384	128	YHL028W	95	0.00072	Saccharomyces cerevisiae	[ui:Yhl028w] [pn:similarity to mucin and other ser-thr rich proteins:hypothetical 63.8 kd protein in gutt-rim1 intergenic region precursor] [gdcf:11.1:5.3] [keggf:14.2] [sgdcf:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4476	25397177_c2_10	6008	20111	1743	581	YHL028W	109	0.0077	Saccharomyces cerevisiae	[ui:Yhl028w] [pn:similarity to mucin and other ser-thr rich proteins:hypothetical 63.8 kd protein in gutt-rim1 intergenic region precursor] [gdcf:11.1:5.3] [keggf:14.2] [sgdcf:9.1.0] [db:gic-saccharomyces cerevisiae]



CONTIG5699	14629382_c1_25	6009	20112	1473	491	YHL028W	153	4.5(10)-8	Saccharomyces cerevisiae	[ui:yh028w] [pn:similarity to mucin and other ser-thr rich proteins:hypothetical 63.8 kd protein in gutt-1 intergenic region precursor] [gtcf:1.1:5.3] [keggfc:14.2] [sgdfc:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1827	35797776_f1_1	6010	20113	342	114	YHL019C	152	5.5(10)-10	Saccharomyces cerevisiae	[ui:yh019c] [pn:involved in clathrin-dependent transport processes:adaplin medium chain homolog] [gn:apn2] [gtcf:1.1:12.16] [keggfc:14.2] [sgdfc:8.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1827	23948587_f1_2	6011	20114	714	238	YHL019C	141	8.4(10)-9	Saccharomyces cerevisiae	[ui:yh019c] [pn:involved in clathrin-dependent transport processes:adaplin medium chain homolog] [gn:apn2] [gtcf:1.1:12.16] [keggfc:14.2] [sgdfc:8.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1827	9805182_f2_3	6012	20115	660	220	YHL019C	130	5.5(10)-6	Saccharomyces cerevisiae	[ui:yh019c] [pn:involved in clathrin-dependent transport processes:adaplin medium chain homolog] [gn:apn2] [gtcf:1.1:12.16] [keggfc:14.2] [sgdfc:8.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1042	23863842_f1_1	6013	20116	825	275	YHL016C	269	4.0(10)-30	Saccharomyces cerevisiae	[ui:yh016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcf:12.4.5.16:1.1] [keggfc:14.2] [sgdfc:1.2.3:1.8.2.7.2.2.9.1.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG3399	2913577_c1_5	6014	20117	819	273	YHL016C	124	7.0(10)-5	Saccharomyces cerevisiae	[ui:yh1016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcf:12.4.5.16:1.1] [kegfc:14.2] [sgdf:1.2.3:1.8.2.7.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG371	6843750_c3_4	6015	20118	1038	346	YHL016C	432	4.4(10)-40	Saccharomyces cerevisiae	[ui:yh1016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcf:12.4.5.16:1.1] [kegfc:14.2] [sgdf:1.2.3:1.8.2.7.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5303	21492838_c2_15	6016	20119	1152	384	YHL016C	527	8.5(10)-51	Saccharomyces cerevisiae	[ui:yh1016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcf:12.4.5.16:1.1] [kegfc:14.2] [sgdf:1.2.3:1.8.2.7.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5355	29344811_f2_1	6017	20120	1512	504	YHL016C	715	1.3(10)-107	Saccharomyces cerevisiae	[ui:yh1016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcf:12.4.5.16:1.1] [kegfc:14.2] [sgdf:1.2.3:1.8.2.7.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5379	10975902_c2_18	6018	20121	2043	681	YHL016C	921	5.9(10)-105	Saccharomyces cerevisiae	[ui:yh1016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcf:12.4.5.16:1.1] [kegfc:14.2] [sgdf:1.2.3:1.8.2.7.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5611	7070305_f1_3	6019	20122	609	203	YHL016C	484	7.2(10)-46	Saccharomyces cerevisiae	[ui:yh016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gfc:12.4.5.16:1.1] [kegfc:14.2] [sgdfc:1.2.3:1.8.2.7.2.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG747	24297337_c3_9	6020	20123	1203	401	YHL016C	507	1.6(10)-48	Saccharomyces cerevisiae	[ui:yh016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gfc:12.4.5.16:1.1] [kegfc:14.2] [sgdfc:1.2.3:1.8.2.7.2.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b9x11469.x	9855416_f3_1	6021	20124	540	180	YHL016C	109	3.0(10)-5	Saccharomyces cerevisiae	[ui:yh016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gfc:12.4.5.16:1.1] [kegfc:14.2] [sgdfc:1.2.3:1.8.2.7.2.2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4312	21673261_f1_1	6022	20125	429	143	YHR096C	183	2.5(10)-13	Saccharomyces cerevisiae	[ui:yr096c] [pn:strong similarity to hexose transporters:probable glucose transporter] [gn:ht5] [gfc:12.2:1.1] [kegfc:14.2] [sgdfc:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4946	2157665_c1_4	6023	20126	417	139	YHR096C	286	1.8(10)-24	Saccharomyces cerevisiae	[ui:yr096c] [pn:strong similarity to hexose transporters:probable glucose transporter] [gn:ht5] [gfc:12.2:1.1] [kegfc:14.2] [sgdfc:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5319	24303912_c1_6	6024	20127	1125	375	YHR096C	334	1.0(10)-29	Saccharomyces cerevisiae	[ui:yr096c] [pn:strong similarity to hexose transporters:probable glucose transporters] [gn:hxt5] [gctc:12.2:1.1] [keggfc:14.2] [sgdfe:1.5.3:7.3.0.8.7.0.9.1.0:17.0.0] [db:gic-saccharomyces cerevisiae]
b3x16095.y	33460818_c2_6	6025	20128	228	76	YIL147C	96	0.00129	Saccharomyces cerevisiae	[ui:yil147c] [pn:two-component signal transducer:osomolarity two-component system protein sh1] [gn:sh1:ypd2] [gctc:12.1:1.1.3:12.13] [ec:2.7.3.-] [keggfc:14.1] [sgdfe:1.5.2:9.1.0:10.3.2:11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2824	23604063_c2_1	6026	20129	1047	349	YIL140W	635	3.1(10)-62	Saccharomyces cerevisiae	[ui:yil140w] [pn:required for axial pattern of budding:ax12 protein precursor:st04 protein] [gn:ax12:st04] [gctc:1.1:1.12.8] [keggfc:14.2] [sgdfe:3.2.0.9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2142	16187630_f2_3	6027	20130	228	76	YIL047C	96	0.00093	Saccharomyces cerevisiae	[ui:yil047c] [pn:member of the major facilitator superfamily:protein] [gn:sgf1] [gctc:1.1.1:12.6:12.8:12.9] [keggfc:14.2] [sgdfe:3.3.0:9.1.0:10.1.6:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3415	19609375_f3_3	6028	20131	1059	353	YIL047C	640	9.1(10)-63	Saccharomyces cerevisiae	[ui:yil047c] [pn:member of the major facilitator superfamily:protein] [gn:sgf1] [gctc:1.1.1:12.6:12.8:12.9] [keggfc:14.2] [sgdfe:3.3.0:9.1.0:10.1.6:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5360	24085326_f3_5	6029	20132	1725	575	YJL028W	1437	3.2(10)-147	Saccharomyces cerevisiae	[ui:yir028w] [pn:allantoin permease:allantoin transport protein] [gn:da14] [gctc:12.6:11.1] [kegfc:14.2] [sgdfe:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3735	13759450_f2_4	6030	20133	633	211	YJL219W	238	2.6(10)-19	Saccharomyces cerevisiae	[ui:yjl219w] [pn:hexose transport protein:hexose transporter hx9] [gn:hx9:j0222:hxc567] [gctc:12.2:11.1] [kegfc:14.2] [sgdfe:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5448	21489688_c1_13	6031	20134	927	309	YJL093C	366	5.7(10)-33	Saccharomyces cerevisiae	[ui:yjl093c] [pn:outward-rectifier potassium channel:outward-rectifier potassium channel tok1:two-domain outward rectifier k+ channel york] [gn:tok1:duk1:j0911] [gctc:11.1:11.3:12.10:12.6] [kegfc:14.2] [sgdfe:1.8.2:7.1.0:8.6.0:9.1.]
CONTIG5448	25813802_c1_12	6032	20135	1287	429	YJL093C	590	1.8(10)-57	Saccharomyces cerevisiae	[ui:yjl093c] [pn:outward-rectifier potassium channel:outward-rectifier potassium channel tok1:two-domain outward rectifier k+ channel york] [gn:tok1:duk1:j0911] [gctc:11.1:11.3:12.10:12.6] [kegfc:14.2] [sgdfe:1.8.2:7.1.0:8.6.0:9.1.]

CONTIG2735	15705057_f2_1	6033	20136	1440	480	YJR040W	320	7.5(10)-28	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:cic-y1:cic-a] [gn:gef1:cley1:j1616] [gtcf:1.1.1.1.3.12.6] [kegfc:14.2] [sgdfe:1.8.2.7.1.0.8.7.0.9.1.0] [db:gtc-saccharomyces cerevis
CONTIG3806	972933_f2_3	6034	20137	465	155	YJR040W	376	6.9(10)-34	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:cic-y1:cic-a] [gn:gef1:cley1:j1616] [gtcf:1.1.1.1.3.12.6] [kegfc:14.2] [sgdfe:1.8.2.7.1.0.8.7.0.9.1.0] [db:gtc-saccharomyces cerevis
CONTIG3806	13850627_f1_2	6035	20138	1248	416	YJR040W	556	7.2(10)-54	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:cic-y1:cic-a] [gn:gef1:cley1:j1616] [gtcf:1.1.1.1.3.12.6] [kegfc:14.2] [sgdfe:1.8.2.7.1.0.8.7.0.9.1.0] [db:gtc-saccharomyces cerevis

CONTIG4484	9781912_c3_7	6036	20139	2466	822	YJR040W	384	2.7(10)-41	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:c1c-y1:c1c-a] [gn:gef1:c1c-y1:j1616] [gtctc:11.1:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gic-saccharomyces cerevis
CONTIG5246	9777082_f3_6	6037	20140	759	253	YJR040W	116	0.00038	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:c1c-y1:c1c-a] [gn:gef1:c1c-y1:j1616] [gtctc:11.1:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gic-saccharomyces cerevis
CONTIG5649	2151425_c1_15	6038	20141	534	178	YJR040W	135	5.2(10)-8	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:c1c-y1:c1c-a] [gn:gef1:c1c-y1:j1616] [gtctc:11.1:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gic-saccharomyces cerevis
CONTIG1183	4871053_f3_1	6039	20142	990	330	YJR151C	148	1.5(10)-7	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, yk1224c, stp1:hyposphinctical 118.4 kd protein in rps7b-dals intergenic region precursor] [gn:j2223] [gtctc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG1562	23641263_c2_4	6040	20143	939	313	YJR151C	92	0.22	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, yk1224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [gtcf:1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG128	14568812_f2_1	6041	20144	402	134	YJR151C	91	0.03699	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, yk1224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [gtcf:1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2535	14884637_f3_3	6042	20145	2490	830	YJR151C	94	0.71999	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, yk1224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [gtcf:1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5387	22667311_f3_11	6043	20146	966	322	YJR151C	106	0.01499	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, yk1224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [gtcf:1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]



CONTIG1416	13704127_c2_5	6044	20147	1374	458	YJR152W	1149	1.0(10)-116	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1;j2230] [gtcf:11.1:12.6] [keggfc:14.2] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1150	26445192_c3_1	6045	20148	774	258	YJR152W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1;j2230] [gtcf:11.1:12.6] [keggfc:14.2] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1605	32078317_f3_1	6046	20149	705	235	YJR152W	562	1.7(10)-54	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1;j2230] [gtcf:11.1:12.6] [keggfc:14.2] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3088	24651561_c1_3	6047	20150	660	220	YJR152W	325	6.5(10)-29	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1;j2230] [gtcf:11.1:12.6] [keggfc:14.2] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5778	24250927_c1_23	6048	20151	1659	553	YJR152W	1205	1.2(10)-122	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1;j2230] [gtcf:11.1:12.6] [keggfc:14.2] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
blx18608.x	6055325_f3_1	6049	20152	189	63	YJR152W	95	0.00063	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1;j2230] [gtcf:11.1:12.6] [keggfc:14.2] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG171	31267580_f2_1	6050	20153	756	252	YKL220C	289	1.3(10)-24	Saccharomyces cerevisiae	[ui:ykl220c] [pn:ferric:and cupric reductase:ferric reductase transmembrane component 2 precursor] [gn:fre2] [gctc:1.1:12.6] [keggfc:14.2] [sgdfe:1.8.1:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4736	7040907_c1_12	6051	20154	1722	574	YKL220C	494	3.2(10)-47	Saccharomyces cerevisiae	[ui:ykl220c] [pn:ferric:and cupric reductase:ferric reductase transmembrane component 2 precursor] [gn:fre2] [gctc:1.1:12.6] [keggfc:14.2] [sgdfe:1.8.1:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1914	20742167_c1_8	6052	20155	549	183	YKL178C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:ykl178c] [pn:pheromone a-factor receptor] [gn:ste3] [gctc:1.1:1.3:12.8:12.9] [keggfc:13.1] [sgdfe:3.0:9.1.0:10.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG1879	1067693_f1_1	6053	20156	633	211	YKR039W	559	3.5(10)-54	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease] [gn:gap1] [gctc:1.1:1.12.1:12.6] [keggfc:14.2] [sgdfe:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG2695	2386458_f2_1	6054	20157	771	257	YKR039W	625	3.5(10)-61	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcf:1.1:1.2.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2933	3908427_f3_1	6055	20158	1038	346	YKR039W	581	1.6(10)-56	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcf:1.1:1.2.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4473	289027_c3_7	6056	20159	702	234	YKR039W	700	4.0(10)-69	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcf:1.1:1.2.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG458	13062660_f1_1	6057	20160	915	305	YKR039W	783	6.2(10)-78	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcf:1.1:1.2.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4723	4879405_fl_1	6058	20161	1527	509	YKR039W	1023	2.2(10)-103	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gfcf:11.1:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gfc-saccharomyces cerevisiae]
CONTIG4899	6147812_c2_9	6059	20162	345	115	YKR039W	108	2.8(10)-5	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gfcf:11.1:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gfc-saccharomyces cerevisiae]
blx18591.y	391899_c1_1	6060	20163	528	176	YKR039W	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gfcf:11.1:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4:0.8:7.0:9.1:0:17.0:0] [db:gfc-saccharomyces cerevisiae]
CONTIG4208	25986017_fl_1	6061	20164	1734	578	YKR050W	871	3.1(10)-129	Saccharomyces cerevisiae	[ui:ykr050w] [pn:moderate-affinity potassium transport protein:potassium transport protein, low-affinity] [gn:trk2.rpd2] [gfcf:12.5:1.1] [kegfc:14.2] [sgdfc:7.2:8.7:0.9.1:0:17.0:0] [db:gfc-saccharomyces cerevisiae]

CONTIG5487	16526511_f2_6	6062	20165	1341	447	YKR050W	391	1.1(10)-39	Saccharomyces cerevisiae	[ui:ykr050w] [pn:moderate-affinity potassium transport protein:potassium transport protein, low-affinity] [gn:irk2:rpdd2] [gicfc:12.5:1.1] [keggfc:14.2] [sgdfe:7.2:2.8:7.0:9.1:0:17.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG4679	25975752_f1_1	6063	20166	624	208	YKR093W	651	6.2(10)-64	Saccharomyces cerevisiae	[ui:ykr093w] [pn:peptide transporter:peptide transporter ptr2:peptide permease ptr2] [gn:ptr2:ykr413] [gicfc:12.1:1.1] [keggfc:14.2] [sgdfe:7.11:0.8:8.0:9.1:0:17.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG4793	10976000_c2_11	6064	20167	963	321	YKR093W	780	1.3(10)-77	Saccharomyces cerevisiae	[ui:ykr093w] [pn:peptide transporter:peptide transporter ptr2:peptide permease ptr2] [gn:ptr2:ykr413] [gicfc:12.1:1.1] [keggfc:14.2] [sgdfe:7.11:0.8:8.0:9.1:0:17.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG4946	15517080_c2_5	6065	20168	816	272	YLR081W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:yhr081w] [pn:galactose and glucose permease:galactose transporter:galactose permease] [gn:gal2:imp1] [gicfc:12.2:1.1:1.6] [keggfc:14.2] [sgdfe:1.5:3:7.3:0.8:7.0:9.1:0:17.0:0] [db:gic-saccharomyces cerevisiae]

CONTIG1005	9886332_fl_1	6066	20169	372	124	YLR081W	157	1.5(10)-10	Saccharomyces cerevisiae	[ui:ylr081w] [pn:galactose and glucose permease:galactose transporter:galactose permease] [gn:gal2:imp1] [gicfc:12.2:11.1:1.6] [keggfc:14.2] [sgdfe:1.5:3:7.3:0.8:7.0:9.1:0:17.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG2624	24225907_fl_2	6067	20170	534	178	YLR110C	138	1.3(10)-9	Saccharomyces cerevisiae	[ui:ylr110c] [pn:putative pseudogene] [gicfc:11.1] [keggfc:14.2] [sgdfe:9.1:0] [db:gic-saccharomyces cerevisiae]
CONTIG2890	1291390_cl_3	6068	20171	1323	441	YLR110C	108	9.3(10)-6	Saccharomyces cerevisiae	[ui:ylr110c] [pn:putative pseudogene] [gicfc:11.1] [keggfc:14.2] [sgdfe:9.1:0] [db:gic-saccharomyces cerevisiae]
CONTIG4658	6503752_fl_3	6069	20172	492	164	YLR229C	645	2.7(10)-63	Saccharomyces cerevisiae	[ui:ylr229c] [pn:gip-binding protein of ras superfamily:cell division control protein 42] [gn:cdc42:src2:18083] [gicfc:11.1:1.3:12.13:12.8:12.9] [keggfc:13.1:13.3] [sgdfe:3.2:0:3.3:0:3.8:0:9.1:0:10.1:2:10.2:3] [db:gic-saccharomyces c
CONTIG4763	11881550_fl_5	6070	20173	198	66	YLR229C	247	4.0(10)-21	Saccharomyces cerevisiae	[ui:ylr229c] [pn:gip-binding protein of ras superfamily:cell division control protein 42] [gn:cdc42:src2:18083] [gicfc:11.1:1.3:12.13:12.8:12.9] [keggfc:13.1:13.3] [sgdfe:3.2:0:3.3:0:3.8:0:9.1:0:10.1:2:10.2:3] [db:gic-saccharomyces c

CONTIG1985	14878405_f2_2	6071	20174	762	254	YLR343W	627	2.2(10)-61	Saccharomyces cerevisiae	[ui:ylr343w] [pn:strong similarity to gas1 p and c.albicans ph responsive protein] [gtcf:1.1.1] [keggfc:14.2] [sgdfe:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3168	20600817_f1_1	6072	20175	1074	358	YLR343W	415	6.2(10)-39	Saccharomyces cerevisiae	[ui:ylr343w] [pn:strong similarity to gas1 p and c.albicans ph responsive protein] [gtcf:1.1.1] [keggfc:14.2] [sgdfe:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2344	12129432_c1_4	6073	20176	1755	585	YML123C	1014	1.5(10)-194	Saccharomyces cerevisiae	[ui:ym123c] [pn:high-affinity inorganic phosphate/h+ symporter:inorganic phosphate transporter pho84] [gn:pho84;ym7056] [gtcf:12.4.1.1.13.10] [keggfc:14.2] [sgdfe:1.4.3.1.8.2.7.2.3.7.3.0.8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG276	14886718_f3_1	6074	20177	573	191	YMR058W	577	4.2(10)-56	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fe3;ym9796] [gtcf:12.6.1.1.3] [keggfc:14.2] [sgdfe:1.8.1.8.7.0.9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4427	4688293_c2_2	6075	20178	1827	609	YMR058W	1480	8.8(10)-152	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fe3;ym9796] [gtcf:12.6.1.1.3] [keggfc:14.2] [sgdfe:1.8.1.8.7.0.9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4629	5351452_c3_9	6076	20179	963	321	YMR058W	910	2.2(10)-91	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gctc:12.6:1.3] [keggtc:14.2] [sgdgc:1.8:1:8.7:0.9:1.0] [db:gct-saccharomyces cerevisiae]
CONTIG5726	25672061_c2_27	6077	20180	1728	576	YMR058W	1658	1.2(10)-170	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gctc:12.6:1.3] [keggtc:14.2] [sgdgc:1.8:1:8.7:0.9:1.0] [db:gct-saccharomyces cerevisiae]
CONTIG806	15041078_f1_1	6078	20181	1179	393	YMR058W	1093	9.0(10)-111	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gctc:12.6:1.3] [keggtc:14.2] [sgdgc:1.8:1:8.7:0.9:1.0] [db:gct-saccharomyces cerevisiae]
CONTIG4895	14570426_f2_2	6079	20182	561	187	YMR183C	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:ymr183c] [pn:involved in vesicle transport from golgi to plasma membrane:sso2 protein] [gn:sso2:ym8010] [gctc:12.6:1.1:12.10:12.16] [keggtc:14.2] [sgdgc:8.3:0.9:1.0] [db:gct-saccharomyces cerevisiae]



CONTIG1375	206887_c1_3	6080	20183	750	250	YMR243C	494	2.7(10)-47	Saccharomyces cerevisiae	[ui:ymr243c] [pn:zinc- and cadmium resistance protein:zinc/cadmium resistance protein] [gn:zrc1:ym9408] [gctc:1.1:1.2:12:12.6] [kegfc:14.2] [sgdfc:1.8:1:7.2:1.8:7.0:9.1:0:11.3:0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5794	24610312_f3_15	6081	20184	771	257	YMR243C	173	2.0(10)-21	Saccharomyces cerevisiae	[ui:ymr243c] [pn:zinc- and cadmium resistance protein:zinc/cadmium resistance protein] [gn:zrc1:ym9408] [gctc:1.1:1.2:12:12.6] [kegfc:14.2] [sgdfc:1.8:1:7.2:1.8:7.0:9.1:0:11.3:0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG2873	7291678_c1_6	6082	20185	735	245	YMR307W	776	3.5(10)-77	Saccharomyces cerevisiae	[ui:ymr307w] [pn:glycophospholipid-anchored surface glycoprotein:glycolipid anchored surface protein precursor:glycoprotein gp115] [gn:gas1:ggp1:ym9952] [gctc:1.1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2446	29320327_c3_9	6083	20186	1590	530	YMR317W	133	2.8(10)-5	Saccharomyces cerevisiae	[ui:ymr317w] [pn:similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase:hyphothetical 113.1 kd protein in pre5-fet4 intergenic region] [gn:ymr316w:ym9924] [gctc:1.1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG3169	10547807_c3_2	6084	20187	1065	355	YMR317W	120	0.00036	Saccharomyces cerevisiae	[ui:ymr317w] [pn:similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase:hypothetical 113.1 kd protein in pre5-fet4 intergenic region] [gn:ymr316w:ym9924] [gicfc:11.1] [keggfc:14.2] [sgdfe:9.1.0] [db:gic-saccharomy
CONTIG2446	9821013_f3_4	6085	20188	597	199	YMR317W	104	0.00979	Saccharomyces cerevisiae	[ui:ymr317w] [pn:similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase:hypothetical 113.1 kd protein in pre5-fet4 intergenic region] [gn:ymr316w:ym9924] [gicfc:11.1] [keggfc:14.2] [sgdfe:9.1.0] [db:gic-saccharomy
CONTIG4341	131306_f3_3	6086	20189	999	333	YNL291C	374	1.7(10)-34	Saccharomyces cerevisiae	[ui:ynl291c] [pn:involved in ca2+ influx during mating:mid1 protein] [gn:mid1.n0530] [gicfc:11.1:12.9] [keggfc:14.2] [sgdfe:3.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4341	22318952_f1_1	6087	20190	738	246	YNL291C	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:ynl291c] [pn:involved in ca2+ influx during mating:mid1 protein] [gn:mid1.n0530] [gicfc:11.1:12.9] [keggfc:14.2] [sgdfe:3.0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4258	35422500_c2_4	6088	20191	702	234	YNL268W	203	1.8(10)-15	Saccharomyces cerevisiae	[ui:ynl268w] [pn:lysine-specific high-affinity permease:lysine-specific permease] [gn:lyp1.n0790] [gicfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfe:1.1:3.7:4.0:8.7:0.9.1.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5516	9787553_c3_17	6089	20192	432	144	YNL268W	150	9.3(10)-10	Saccharomyces cerevisiae	[ui:ynl268w] [pn:lysine-specific high-affinity permease:lysine-specific permease] [gn:lyp1:n0790] [gctc:1.1:12.1:12.6] [keggct:14.2] [sgdct:1.1:3:7.4:0.8:7.0:9.1:0:17.0.0] [db:gct-saccharomyces cerevisiae]
CONTIG4856	35425753_c2_11	6090	20193	723	241	YNL142W	555	9.1(10)-54	Saccharomyces cerevisiae	[ui:ynl142w] [pn:high affinity low capacity ammonia permease:ammonium transporter mep2] [gn:mep2:n1207:n1820] [gctc:12.5:1.1] [keggct:14.2] [sgdct:1.2:3:7.2:2.8:7.0:9.1:0:17.0.0] [db:gct-saccharomyces cerevisiae]
CONTIG3294	23885417_f3_1	6091	20194	231	77	YNL142W	123	5.5(10)-7	Saccharomyces cerevisiae	[ui:ynl142w] [pn:high affinity low capacity ammonia permease:ammonium transporter mep2] [gn:mep2:n1207:n1820] [gctc:12.5:1.1] [keggct:14.2] [sgdct:1.2:3:7.2:2.8:7.0:9.1:0:17.0.0] [db:gct-saccharomyces cerevisiae]
CONTIG5673	23944050_f3_22	6092	20195	387	129	YNL142W	297	5.7(10)-26	Saccharomyces cerevisiae	[ui:ynl142w] [pn:high affinity low capacity ammonia permease:ammonium transporter mep2] [gn:mep2:n1207:n1820] [gctc:12.5:1.1] [keggct:14.2] [sgdct:1.2:3:7.2:2.8:7.0:9.1:0:17.0.0] [db:gct-saccharomyces cerevisiae]

CONTIG2519	972775_c2_3	6093	20196	492	164	YNR044W	92	0.0019	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:11.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3537	7119442_f2_1	6094	20197	2055	685	YNR044W	177	4.2(10)-10	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:11.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3914	16438431_f2_1	6095	20198	666	222	YNR044W	93	0.11	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:11.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4784	19707027_f2_5	6096	20199	1305	435	YNR044W	104	0.02199	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:11.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4984	979811_c2_10	6097	20200	666	222	YNR044W	98	0.033	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:11.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5771	7223407_f2_14	6098	20201	2118	706	YNR044W	122	0.00054	Saccharomyces cerevisiae	[ui:ym044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:1.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
b2x16511.y	19800668_c3_3	6099	20202	645	215	YNR044W	124	1.6(10)-5	Saccharomyces cerevisiae	[ui:ym044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n3431] [gtcf:1.1:12.9] [kegfc:14.2] [sgdfc:3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
b1x11922.y	12225262_f3_2	6100	20203	213	71	YOL103W	125	4.5(10)-7	Saccharomyces cerevisiae	[ui:yol103w] [pn:myo-inositol permease, minor:myo-inositol transporter 2] [gn:it2:htb612] [gtcf:12.2:1.1:8.2] [kegfc:14.2] [sgdfc:1.5:3.7:3.0:8.7:0.9:1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5391	22269681_f2_7	6101	20204	1365	455	YOL030W	727	5.5(10)-72	Saccharomyces cerevisiae	[ui:yol030w] [pn:strong similarity to glycoprotein gas1] [gtcf:1.1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	14082032_c1_28	6102	20205	1458	486	YOL030W	1139	1.2(10)-115	Saccharomyces cerevisiae	[ui:yol030w] [pn:strong similarity to glycoprotein gas1] [gtcf:1.1.1] [kegfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1804	2165682_f3_1	6103	20206	357	119	YOR153W	231	7.0(10)-18	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pd15:stf:ydr1:lem1] [gtcf:1.1:12.12:12.6] [kegfc:14.2] [sgdfc:7.9:0:9.1.0:1.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2003	19730018_c2_1	6104	20207	1476	492	YOR153W	1295	3.5(10)-132	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pd5:sis1:ydr1:lem1] [gctc:1.1:1.2:12:12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0:1.1.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3893	3912700_c1_4	6105	20208	213	71	YOR153W	136	9.1(10)-8	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pd5:sis1:ydr1:lem1] [gctc:1.1:1.2:12:12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0:1.1.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3893	24409837_c3_5	6106	20209	1182	394	YOR153W	1064	2.2(10)-107	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pd5:sis1:ydr1:lem1] [gctc:1.1:1.2:12:12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0:1.1.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4325	10944062_c2_4	6107	20210	2085	695	YOR153W	1839	7.9(10)-190	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pd5:sis1:ydr1:lem1] [gctc:1.1:1.2:12:12.6] [kegfc:14.2] [sgdfe:7.9.0:9.1.0:1.1.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4513	9776886_c2_10	6108	20211	1878	626	YOR153W	1513	2.7(10)-155	Saccharomyces cerevisiae	[ui.yor153w] [pn.pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn.pdr5:sis1.ydr1:lem1] [gtcf:11.1:12.12:12.6] [kegfc:14.2] [sgdc:7.9.0:9.1.0:1.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG5733	34407687_f3_14	6109	20212	2223	741	YOR153W	1927	3.7(10)-199	Saccharomyces cerevisiae	[ui.yor153w] [pn.pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn.pdr5:sis1.ydr1:lem1] [gtcf:11.1:12.12:12.6] [kegfc:14.2] [sgdc:7.9.0:9.1.0:1.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG3215	1056349_c1_4	6110	20213	723	241	YOR153W	180	1.8(10)-12	Saccharomyces cerevisiae	[ui.yor153w] [pn.pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn.pdr5:sis1.ydr1:lem1] [gtcf:11.1:12.12:12.6] [kegfc:14.2] [sgdc:7.9.0:9.1.0:1.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG4724	2353769_c1_5	6111	20214	1809	603	YOR153W	1786	3.2(10)-184	Saccharomyces cerevisiae	[ui.yor153w] [pn.pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn.pdr5:sis1.ydr1:lem1] [gtcf:11.1:12.12:12.6] [kegfc:14.2] [sgdc:7.9.0:9.1.0:1.3.0] [db:glc-saccharomyces cerevisiae]

CONTIG5164	30548253_f3_4	6112	20215	1215	405	YOR212W	371	1.8(10)-68	Saccharomyces cerevisiae	[ui:yor212w] [pn:gtp-binding protein beta subunit of the pheromone pathway:guanine nucleotide-binding protein beta subunit] [gn:ste4:yor50-2] [gicfc:1.1.1.1.3.12.13.12.8.12.9] [keggfc:13.1] [sgdfe:3.3.0.9.1.0.10.1.2] [db:gic-saccharom
CONTIG5164	20157626_f1_2	6113	20216	303	101	YOR212W	212	8.3(10)-17	Saccharomyces cerevisiae	[ui:yor212w] [pn:gtp-binding protein beta subunit of the pheromone pathway:guanine nucleotide-binding protein beta subunit] [gn:ste4:yor50-2] [gicfc:1.1.1.1.3.12.13.12.8.12.9] [keggfc:13.1] [sgdfe:3.3.0.9.1.0.10.1.2] [db:gic-saccharom
CONTIG1479	10437713_f1_1	6114	20217	867	289	YOR328W	627	4.5(10)-60	Saccharomyces cerevisiae	[ui:yor328w] [pn:strong similarity to abc transporter proteins:atp-dependent permease] [gn:ptr10] [gicfc:12.6.1.1.1] [keggfc:14.2] [sgdfe:7.9.0.9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5548	962511_f3_7	6115	20218	1452	484	YOR348C	613	6.5(10)-60	Saccharomyces cerevisiae	[ui:yor348c] [pn:proline and gamma-aminobutyrate permease] [gn:put4:o6345] [gicfc:11.1.1.12.1.12.6] [keggfc:14.2] [sgdfe:1.1.3.7.4.0.8.7.0.9.1.0.17.0.0] [db:gic-saccharomyces cerevisiae]



CONTIG1316	20706716_f1_1	6116	20219	1185	395	YPL176C	520	1.1(10)-49	Saccharomyces cerevisiae	[ui:yp1176c] [pn:similarity to chinese hamster transferrin receptor protein] [gtcf:1.1:14.3] [keggf:14.2] [sgdfc:9.1.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2272	11172192_f2_1	6117	20220	183	61	YPL036W	207	1.3(10)-15	Saccharomyces cerevisiae	[ui:yp1036w] [pn:h+-transporting p-type atpase 2; plasma membrane atpase 2; proton pump] [gn:pna2] [gtcf:12.5:1.1] [ec:3.6.1.35] [keggf:14.1] [sgdfc:1.8.2:7.2:7.8.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4917	3941881_g3_7	6118	20221	765	255	YPR124W	155	1.3(10)-10	Saccharomyces cerevisiae	[ui:yp124w] [pn:copper transport protein:copper transport protein ctrl:copper transporter 1] [gn:ctrl:p9642] [gtcf:12.6:1.1] [keggf:14.2] [sgdfc:1.8.1:7.2.1.8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3571	3917188_g2_6	6119	20222	1317	439	YGR217W	696	3.5(10)-67	Saccharomyces cerevisiae	[ui:yg217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpi1-erm1 intergenic region] [gn:ochl:g8501] [gtcf:1.3:12.6] [keggf:14.2] [sgdfc:1.8.2:7.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG977	3380130_f1_1	6120	20223	1158	386	YGR217W	769	5.7(10)-75	Saccharomyces cerevisiae	[ui:yg217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpi1-erm1 intergenic region] [gn:ochl:g8501] [gtcf:1.3:12.6] [keggf:14.2] [sgdfc:1.8.2:7.1.0] [db:gtc-saccharomyces cerevisiae]

b1x18140.x	22447143_f3_2	6121	20224	804	268	YGR217W	328	5.0(10)-28	Saccharomyces cerevisiae	[ui:ygr217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpi1-erm1 intergenic region] [gn:ech1:g8501] [gicfc:1.3:12.6] [kegfc:14.2] [sgdfe:1.8:2.7.1.0] [db:gic-saccharomyces cerevisiae]
b1x18140.y	26348125_c3_3	6122	20225	699	233	YGR217W	99	0.1	Saccharomyces cerevisiae	[ui:ygr217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpi1-erm1 intergenic region] [gn:ech1:g8501] [gicfc:1.3:12.6] [kegfc:14.2] [sgdfe:1.8:2.7.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5158	13985377_f2_4	6123	20226	375	125	YLL053C	330	6.4(10)-30	Saccharomyces cerevisiae	[ui:yll053c] [pn:similarity to water channel proteins] [gicfc:1.3:12.6] [kegfc:14.2] [sgdfe:7.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4438	9814667_c3_9	6124	20227	1134	378	YHR146W	145	3.0(10)-7	Saccharomyces cerevisiae	[ui:yhr146w] [pn:similarity to pheromone-response g-protein mdc1:p:hypothetical 51.1 kd protein in dcd1-mrp6 intergenic region] [gicfc:1.3:12.13:12.9] [kegfc:14.2] [sgdfe:3.0:10.1.2] [db:gic-saccharomyces cerevisiae]
CONTIG4396	406591_f3_7	6125	20228	1239	413	YNL173C	220	2.0(10)-16	Saccharomyces cerevisiae	[ui:ynl173c] [pn:gtp-binding protein of the pheromone-response pathway:hypothetical 40.3 kd protein in rps3-psd1 intergenic region] [gn:mdg1:n1673] [gicfc:1.3:12.13:12.9] [kegfc:14.2] [sgdfe:3.0:10.1.2] [db:gic-saccharomyces cerevisiae]

CONTIG3561	5994582_f3_2	6126	20229	1671	557	YCR032W	791	3.0(10)-77	Saccharomyces cerevisiae	[ui:ycr032w] [pn:similarity to human cdc41 protein:hyprothetical 251.0 kd protein in cry1-gns1 intergenic region] [gn:ycr32w:ycr591:ycr601] [gtcf:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4746	892153_g3_14	6127	20230	2970	990	YCR032W	131	0.00032	Saccharomyces cerevisiae	[ui:ycr032w] [pn:similarity to human cdc41 protein:hyprothetical 251.0 kd protein in cry1-gns1 intergenic region] [gn:ycr32w:ycr591:ycr601] [gtcf:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3820	22039002_f1_1	6128	20231	1134	378	YDR129C	1396	7.0(10)-143	Saccharomyces cerevisiae	[ui:ydr129c] [pn:actin filament bundling protein, fimbrin:fimbrin:abp67] [gn:sac6:yd9302] [gtcf:12.10:12.16:12.6:12.8] [keggfc:14.2] [sgdfc:3.2.0:8.6.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x12817.x	12206280_f3_2	6129	20232	552	184	YDR129C	511	4.2(10)-49	Saccharomyces cerevisiae	[ui:ydr129c] [pn:actin filament bundling protein, fimbrin:fimbrin:abp67] [gn:sac6:yd9302] [gtcf:12.10:12.16:12.6:12.8] [keggfc:14.2] [sgdfc:3.2.0:8.6.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4074	5939791_f3_2	6130	20233	1323	441	YDR164C	404	5.7(10)-50	Saccharomyces cerevisiae	[ui:ydr164c] [pn:protein transport protein:protein transport protein sec1] [gn:sec1:ydr358] [gctc:12.6:12.10] [keggfc:14.2] [sgdfe:8.6:0.9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5623	21675306_f2_3	6131	20234	2919	973	YDR166C	167	4.4(10)-13	Saccharomyces cerevisiae	[ui:ydr166c] [pn:required for exocytosis] [gn:sec5] [gctc:12.10] [keggfc:14.2] [sgdfe:8.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG5659	12897311_f1_5	6132	20235	1596	532	YER006W	1169	7.0(10)-132	Saccharomyces cerevisiae	[ui:yer006w] [pn:similarity to p.polycephalum myosin-related protein mlpa:hypothetical gfp-binding protein in pm140-pac2 intergenic region] [gctc:12.10] [keggfc:14.2] [sgdfe:8.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG4180	23475013_f1_1	6133	20236	1008	336	YER008C	110	0.0082	Saccharomyces cerevisiae	[ui:yer008c] [pn:secretory pathway protein:sec3 protein:psl1 protein] [gn:sec3:psl1] [gctc:12.10] [keggfc:14.2] [sgdfe:8.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG4682	4085302_c2_9	6134	20237	1971	657	YER008C	195	8.9(10)-14	Saccharomyces cerevisiae	[ui:yer008c] [pn:secretory pathway protein:sec3 protein:psl1 protein] [gn:sec3:psl1] [gctc:12.10] [keggfc:14.2] [sgdfe:8.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG2338	10156251_f1_2	6135	20238	1269	423	YER136W	1450	1.3(10)-148	Saccharomyces cerevisiae	[ui:yer136w] [pn:gdp dissociation inhibitor:secretory pathway gdp dissociation inhibitor] [gn:gdt1:sec19] [gctc:12.10] [keggfc:14.2] [sgdfe:8.6:0.9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG3542	2383456_f3_5	6136	20239	240	80	YER136W	243	3.7(10)-20	Saccharomyces cerevisiae	[ui:yer136w] [pn:gdp dissociation inhibitor:secretory pathway gdp dissociation inhibitor] [gn:gd1:sec19] [gtcf:12.10] [keggfc:14.2] [sgdfc:8.6.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1785	14219066_f2_4	6137	20240	513	171	YIL068C	134	7.0(10)-8	Saccharomyces cerevisiae	[ui:yil068c] [pn:protein transport protein] [gn:sec6] [gtcf:12.6:12.10] [keggfc:14.2] [sgdfc:8.6.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG910	19697067_f2_1	6138	20241	1152	384	YIL068C	154	8.9(10)-8	Saccharomyces cerevisiae	[ui:yil068c] [pn:protein transport protein] [gn:sec6] [gtcf:12.6:12.10] [keggfc:14.2] [sgdfc:8.6.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5737	33707175_f1_1	6139	20242	1839	613	YIL085W	206	1.8(10)-13	Saccharomyces cerevisiae	[ui:yil085w] [pn:70 kda exocyst component protein:hyppothetical 71.3 kd protein in trl1-act3 intergenic region] [gn:exo70:j0932] [gtcf:14.1] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4522	29382768_c3_7	6140	20243	1569	523	YIL044C	96	0.13	Saccharomyces cerevisiae	[ui:yil044c] [pn:glpase-activating protein:glpase-activating protein of ypl6] [gn:gyo6:j1202] [gtcf:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2964	7070336_c3_1	6141	20244	1752	584	YKL212W	1297	2.2(10)-132	Saccharomyces cerevisiae	[ui:ykl212w] [pn:recessive suppressor of secretory defect] [gn:rsd1:sac1] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:8.6.0.9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5676	12145181_f2_7	6142	20245	2385	795	YLR166C	580	1.6(10)-103	Saccharomyces cerevisiae	[ui:ylr166c] [pn:required for exocytosis] [gn:sec10] [gicfc:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2088	25657775_c1_4	6143	20246	387	129	YLR250W	209	4.2(10)-17	Saccharomyces cerevisiae	[ui:ylr250w] [pn:secretory protein:protein ssp120 precursor] [gn:ssp120:19672] [gicfc:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5628	35351442_f3_7	6144	20247	285	95	YLR250W	171	4.5(10)-13	Saccharomyces cerevisiae	[ui:ylr250w] [pn:secretory protein:protein ssp120 precursor] [gn:ssp120:19672] [gicfc:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1601	26692655_c3_4	6145	20248	576	192	YMR308C	286	6.2(10)-24	Saccharomyces cerevisiae	[ui:ymr308c] [pn:protein secretion enhancer:protein secretion enhancer 1] [gn:pse1:ym9952] [gicfc:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4469	20523407_c3_9	6146	20249	1710	570	YMR308C	1423	9.5(10)-146	Saccharomyces cerevisiae	[ui:ymr308c] [pn:protein secretion enhancer:protein secretion enhancer 1] [gn:pse1:ym9952] [gicfc:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gtc-saccharomyces cerevisiae]
blx11465.y	5948958_f1_1	6147	20250	690	230	YMR308C	465	4.2(10)-43	Saccharomyces cerevisiae	[ui:ymr308c] [pn:protein secretion enhancer:protein secretion enhancer 1] [gn:pse1:ym9952] [gicfc:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2985	29298752_c2_6	6148	20251	924	308	YNL325C	112	0.00209	Saccharomyces cerevisiae	[ui:ynl325c] [pn:suppressor of sac1 mutation:hypothetical 101.7 kd protein in egf2-kre1 intergenic region] [gn:n0330] [gtcf:14.1] [kegfc:14.2] [sgdfc:8.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG2985	36114765_c1_5	6149	20252	954	318	YNL325C	917	4.0(10)-92	Saccharomyces cerevisiae	[ui:ynl325c] [pn:suppressor of sac1 mutation:hypothetical 101.7 kd protein in egf2-kre1 intergenic region] [gn:n0330] [gtcf:14.1] [kegfc:14.2] [sgdfc:8.6.0] [db:gic-saccharomyces cerevisiae]
b1x17759.y	36586066_c3_1	6150	20253	477	159	YNL325C	281	1.5(10)-23	Saccharomyces cerevisiae	[ui:ynl325c] [pn:suppressor of sac1 mutation:hypothetical 101.7 kd protein in egf2-kre1 intergenic region] [gn:n0330] [gtcf:14.1] [kegfc:14.2] [sgdfc:8.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5643	10720437_f1_1	6151	20254	780	260	YNL036W	344	2.1(10)-31	Saccharomyces cerevisiae	[ui:ynl036w] [pn:involved in non-classical protein export pathway:non-classical export protein nce3] [gn:nce3:n2695] [gtcf:12.10] [kegfc:14.2] [sgdfc:8.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5697	24097192_c1_16	6152	20255	552	184	YNR049C	114	8.1(10)-7	Saccharomyces cerevisiae	[ui:ynr049c] [pn:secretion protein, multicopy suppressor of sec1:msol protein] [gn:msol:n3457] [gtcf:12.10] [kegfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5397	21650312_f1_2	6153	20256	1575	525	YOR307C	677	1.1(10)-66	Saccharomyces cerevisiae	[ui:yor307c] [pn:secretory pathway protein:sly41 protein] [gn:sly41:o5663] [gtcf:12.10] [kegfc:14.2] [sgdfe:8.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4631	10603402_c2_9	6154	20257	567	189	YOR326W	654	6.0(10)-63	Saccharomyces cerevisiae	[ui:yor326w] [pn:myosin heavy chain:myosin-2 isoform] [gn:myo2.cdcd66.o6167] [gtcf:12.10:12.16:12.8] [kegfc:14.2] [sgdfe:3.2.0:8.3.0:8.6.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4823	23938942_c3_11	6155	20258	3783	1261	YOR326W	2317	1.8(10)-240	Saccharomyces cerevisiae	[ui:yor326w] [pn:myosin heavy chain:myosin-2 isoform] [gn:myo2.cdcd66.o6167] [gtcf:12.10:12.16:12.8] [kegfc:14.2] [sgdfe:3.2.0:8.3.0:8.6.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4917	1064138_f3_2	6156	20259	2439	813	YPR055W	180	9.5(10)-35	Saccharomyces cerevisiae	[ui:yp055w] [pn:protein transport protein:protein transport protein sec8] [gn:sec8.ypr499] [gtcf:12.6:12.10] [kegfc:14.2] [sgdfe:8.6.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4917	2350017_f3_3	6157	20260	378	126	YPR055W	143	1.1(10)-8	Saccharomyces cerevisiae	[ui:yp055w] [pn:protein transport protein:protein transport protein sec8] [gn:sec8.ypr499] [gtcf:12.6:12.10] [kegfc:14.2] [sgdfe:8.6.0:9.2.0] [db:gic-saccharomyces cerevisiae]



CONTIG3891	29393826_c1_6	6158	20261	444	148	YPR149W	165	2.0(10)-12	Saccharomyces cerevisiae	[ui:ypri49w] [pn:involved in non-classical protein export pathway] [gn:nce2] [gtcf:12.10] [kegfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5307	19531308_c2_8	6159	20262	918	306	YBL050W	582	1.3(10)-56	Saccharomyces cerevisiae	[ui:ybl050w] [pn:transport vesicle fusion protein:vesicular-fusion protein sec17] [gn:sec17.yb0517.yb0505] [gtcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
b3x13161.x	11182317_f1_1	6160	20263	489	163	YDL195W	359	1.3(10)-31	Saccharomyces cerevisiae	[ui:ydl195w] [pn:component of the copii coat of er-golgi vesicles:web1 protein:protein transport protein sec31] [gn:web1.sec31.d1229] [gtcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5234	6674055_c2_14	6161	20264	558	186	YDL192W	764	6.5(10)-76	Saccharomyces cerevisiae	[ui:ydl192w] [pn:gtp-binding protein of the arf family:adp-ribosylation factor 1] [gn:arf1.d1244] [gtcf:12.10:12.16] [kegfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5563	36362925_c3_27	6162	20265	321	107	YDL192W	410	2.1(10)-38	Saccharomyces cerevisiae	[ui:ydl192w] [pn:gtp-binding protein of the arf family:adp-ribosylation factor 1] [gn:arf1.d1244] [gtcf:12.10:12.16] [kegfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2659	23439003_c2_2	6163	20266	1350	450	YDL145C	752	1.2(10)-85	Saccharomyces cerevisiae	[ui:ydl145c] [pn:coatomer complex alpha chain of secretory pathway vesicles:coatomer alpha subunit:alpha-coat protein:alpha-cop] [gn:retl:d1578] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4447	4328801_f3_3	6164	20267	2187	729	YDL145C	2630	1.2(10)-273	Saccharomyces cerevisiae	[ui:ydl145c] [pn:coatomer complex alpha chain of secretory pathway vesicles:coatomer alpha subunit:alpha-coat protein:alpha-cop] [gn:retl:d1578] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5563	4866425_c3_28	6165	20268	204	68	YDL137W	250	1.8(10)-21	Saccharomyces cerevisiae	[ui:ydl137w] [pn:gip-binding protein of the arf family:adp-ribosylation factor 2] [gn:arf2:d2165] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG2554	2156312_c1_2	6166	20269	1245	415	YDL058W	91	0.77	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcf:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG2678	964037_c3_7	6167	20270	1548	516	YDL058W	132	6.5(10)-5	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcfc:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4025	3944642_f1_1	6168	20271	1020	340	YDL058W	160	2.7(10)-9	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcfc:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4561	19647768_c1_7	6169	20272	2535	845	YDL058W	157	1.3(10)-7	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcfc:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4748	34554182_f3_6	6170	20273	480	160	YDL058W	435	1.7(10)-39	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcfc:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]

CONTIG4748	2212527_f3_7	6171	20274	723	241	YDL058W	421	5.2(10)-38	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4925	31463538_f2_2	6172	20275	1893	631	YDL058W	206	8.0(10)-13	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5390	860677_g3_18	6173	20276	2454	818	YDL058W	142	8.9(10)-6	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5559	50000_c1_15	6174	20277	1827	609	YDL058W	117	0.00459	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfc:8.3:0.9:4.0] [db:gic-saccharomyces cerevisiae]

CONTIG5652	33994130_f3_12	6175	20278	1977	659	YDL058W	179	1.2(10)-9	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5660	10425152_c1_17	6176	20279	1347	449	YDL058W	242	6.5(10)-17	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5700	36621337_f2_7	6177	20280	2241	747	YDL058W	110	0.024	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5758	32116327_c2_18	6178	20281	2433	811	YDL058W	298	2.1(10)-22	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]

b3x19231.y	22878150_f1_1	6179	20282	477	159	YDL058W	90	0.17	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfe:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG1488	860799_c1_2	6180	20283	1152	384	YDL058W	93	0.60999	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfe:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5228	4385144_c2_8	6181	20284	3237	1079	YDL058W	766	1.8(10)-96	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfe:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
b2x13809.x	26571937_c1_1	6182	20285	516	172	YDR107C	288	1.5(10)-24	Saccharomyces cerevisiae	[ui:ydr107c] [pn:strong similarity to emp70 protein] [gtcf:12.10:12.16] [kegfc:14.2] [sgdfe:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4535	16048313_c1_5	6183	20286	1215	405	YDR170C	95	0.14	Saccharomyces cerevisiae	[ui:ydr170c] [pn:component of non-clathrin vesicle coat:protein transport protein] [gn:sec7] [gtcf:12.6:12.10:12.16] [kegfc:14.2] [sgdfe:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]

b1x18043.x	23495188_c2_2	6184	20287	540	180	YDR170C	326	5.0(10)-29	Saccharomyces cerevisiae	[ui:ydr170c] [pn:component of non-clathrin vesicle coat:protein transport protein] [gn:sec7] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5794	10552186_c3_37	6185	20288	1938	646	YDR189W	1523	2.3(10)-156	Saccharomyces cerevisiae	[ui:ydr189w] [pn:hydrophilic suppressor of ypt1 and member of the sec1p family:sly1 protein] [gn:sly1:ydr9395] [gctc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5526	23864032_f1_2	6186	20289	2889	963	YDR238C	2373	2.1(10)-246	Saccharomyces cerevisiae	[ui:ydr238c] [pn:coatamer complex beta chain of secretory pathway vesicles:coatamer beta subunit:beta-coat protein:beta-cop] [gn:sec26:ydr8419] [gctc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5591	26250462_c1_9	6187	20290	1956	652	YEL022W	412	8.8(10)-43	Saccharomyces cerevisiae	[ui:yel022w] [pn:gdp/gtp exchange factor for arfhypothetical 165.7 kd protein in rip1-ura3 intergenic region] [gn:gea2] [gctc:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4337	20906375_f2_2	6188	20291	684	228	YFL038C	807	1.8(10)-80	Saccharomyces cerevisiae	[ui:yfl038c] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt1:protein ypt2] [gn:ypt1:ypt2] [gctc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gic-saccharomyces cerevisiae]

b3x12764.y	33363252_c3_2	6189	20292	504	168	YFL025C	243	2.2(10)-19	Saccharomyces cerevisiae	[ui:yf025c] [pn:negative regulator of copii vesicle formation:hyphothetical 117.8 kd protein in ste2-frs2 intergenic region] [gn:bsl1] [gctc:12.13] [keggfc:14.2] [sgdfe:8.3.0.9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4023	4331311_c1_5	6190	20293	642	214	YFL005W	661	5.4(10)-65	Saccharomyces cerevisiae	[ui:yf005w] [pn:gip-binding protein of the ras superfamily:ras-related protein] [gn:sec4] [gctc:12.10.12.16] [keggfc:14.2] [sgdfe:8.3.0.9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5218	6454378_c2_11	6191	20294	423	141	YFL005W	93	0.0015	Saccharomyces cerevisiae	[ui:yf005w] [pn:gip-binding protein of the ras superfamily:ras-related protein] [gn:sec4] [gctc:12.10.12.16] [keggfc:14.2] [sgdfe:8.3.0.9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5633	19553200_c3_20	6192	20295	1767	589	YFR051C	451	4.7(10)-82	Saccharomyces cerevisiae	[ui:yf051c] [pn:coatomer complex delta chain:coatomer delta subunit:delta-coat protein:delta-cop] [gn:ret2] [gctc:12.10.12.16] [keggfc:14.2] [sgdfe:8.3.0.9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4965	11975878_c3_8	6193	20296	1359	453	YGL225W	861	3.3(10)-86	Saccharomyces cerevisiae	[ui:ygl225w] [pn:vanadate-resistance protein:gog5/vrg4/van2] [gn:gog5:vrg4:van2] [gctc:12.10.12.16] [keggfc:14.2] [sgdfe:8.3.0.9.4.0] [db:gic-saccharomyces cerevisiae]



CONTIG1396	33360718_f2_1	6194	20297	414	138	YGL210W	411	1.7(10)-38	Saccharomyces cerevisiae	[ui:ycl210w] [pn:small gtp-binding protein essential for golgi function:gtp-binding protein ypt32ypt11] [gn:ypt32ypt11] [gicfc:12.10] [keggfc:14.2] [sgdfe:8.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG1276	4382688_f1_1	6195	20298	639	213	YGL200C	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:ycl200c] [pn:component of the copii-coated vesicles, 24 kda:endosomal p24b protein precursor:24 kd endomembrane protein:basic 24 kd late endocytic intermediate component] [gn:emp24:g1271] [gicfc:12.10:12.16] [keggfc:14.2] [sgdfe:8
CONTIG379	33234688_f2_1	6196	20299	492	164	YGL167C	169	1.6(10)-11	Saccharomyces cerevisiae	[ui:ycl167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pmr1:sccl:bsd1:g1666] [gicfc:12.5:12.10:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:1.8.2:7.2.2:7.8.0:8.3.0:9.4.0] [db:gic-saccharomyc
CONTIG3803	26609812_c3_7	6197	20300	1005	335	YGL167C	930	1.7(10)-93	Saccharomyces cerevisiae	[ui:ycl167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pmr1:sccl:bsd1:g1666] [gicfc:12.5:12.10:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:1.8.2:7.2.2:7.8.0:8.3.0:9.4.0] [db:gic-saccharomyc

CONTIG4780	14167037_c2_9	6198	20301	225	75	YGL167C	110	3.2(10)-5	Saccharomyces cerevisiae	[ui:yg1167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pnrl:sccl:bsd1:g1666] [gctfc:12.5:12.10:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:1.8.2:7.2:7.8.0:8.3.0:9.4.0] [db:gic-saccharomyc
CONTIG5017	32132212_c3_8	6199	20302	1158	386	YGL167C	836	1.5(10)-83	Saccharomyces cerevisiae	[ui:yg1167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pnrl:sccl:bsd1:g1666] [gctfc:12.5:12.10:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:1.8.2:7.2:7.8.0:8.3.0:9.4.0] [db:gic-saccharomyc
CONTIG4235	20524127_c3_6	6200	20303	1443	481	YGL145W	121	0.00042	Saccharomyces cerevisiae	[ui:yg1145w] [pn:required for er to golgi transport:protein transport protein tip20] [gn:tip20:tip1] [gctfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfe:8.3.0:9.4.0] [db:gic-saccharomycs cerevisiae]
CONTIG3846	4884437_c3_2	6201	20304	1728	576	YGL137W	1848	8.8(10)-191	Saccharomyces cerevisiae	[ui:yg1137w] [pn:coatomer complex beta" chain:beta"cop of secretory pathway vesicles:coatomer beta" subunit:beta"-coat protein:beta"-cop] [gn:sec27:g2827] [gctfc:12.10:12.16] [keggfc:14.2] [sgdfe:8.3.0:9.9.0] [db:gic-saccharomycs c

CONTIG4593	7083401_c2_4	6202	20305	834	278	YGL137W	340	7.2(10)-30	Saccharomyces cerevisiae	[ui:yl137w] [pn:coatomer complex beta" chain:beta"-cop of secretory pathway vesicles:coatomer beta" subunit:beta"-coat protein:beta"-cop] [gn:sec27.g2827] [gtcf:12.10:12.16] [keggf:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces c
CONTIG4500	21722675_f1_1	6203	20306	732	244	YGR167W	295	3.2(10)-26	Saccharomyces cerevisiae	[ui:yl167w] [pn:clathrin light chain:clc] [gn:clc1] [gtcf:12.10:12.6:12.8] [keggf:14.2] [sgdfc:3.1.0:8.3.0:8.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4504	4862510_f2_1	6204	20307	483	161	YIL004C	129	1.3(10)-8	Saccharomyces cerevisiae	[ui:yl004c] [pn:protein transport protein:protein transport protein bet1:protein sly12] [gn:bet1.sly12.yia4c] [gtcf:12.6:12.10:12.16] [keggf:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4702	25431318_c2_6	6205	20308	402	134	YKR068C	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:yl068c] [pn:involved in targeting and fusion of er to golgi transport vesicles:hypothetical 22.1 kd protein in cpl1-sis2 intergenic region] [gn:bet3] [gtcf:12.6:12.10:12.16] [keggf:14.2] [sgdfc:8.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3236	4151525_f1_1	6206	20309	570	190	YLR026C	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:yl026c] [pn:syntaxin:tsnae:integral membrane protein] [gn:sed5] [gtcf:12.10:12.16] [keggf:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4698	10210151_c2_5	6207	20310	750	250	YLR078C	377	6.7(10)-35	Saccharomyces cerevisiae	[ui:y t078c] [pn:weak similarity to synaptoobrevin.v-snare:vesicular transport protein bos1] [gn:bosl:19449] [gtcf:12.6:12.10:12.16] [keggfc:14.2] [sgdfe:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2154	398885_f2_3	6208	20311	726	242	YLR083C	656	1.8(10)-64	Saccharomyces cerevisiae	[ui:y t083c] [pn:endosomal protein:endosomal p24a protein precursor:70 kd endomembrane protein:pheromone alpha-factor transporter:acidic 24 kd late endocytic intermediate component] [gn:emp70] [gtcf:12.6:12.9:12.10:12.16] [keggfc:14.
b2x13809.x	15674131_c3_3	6209	20312	213	71	YLR083C	159	1.1(10)-10	Saccharomyces cerevisiae	[ui:y t083c] [pn:endosomal protein:endosomal p24a protein precursor:70 kd endomembrane protein:pheromone alpha-factor transporter:acidic 24 kd late endocytic intermediate component] [gn:emp70] [gtcf:12.6:12.9:12.10:12.16] [keggfc:14.
CONTIG5814	4412642_c3_63	6210	20313	843	281	YLR093C	149	9.1(10)-9	Saccharomyces cerevisiae	[ui:y t093c] [pn:weak similarity to synaptoobrevin] [gtcf:12.10] [keggfc:14.2] [sgdfe:8.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5059	29345400_f2_2	6211	20314	912	304	YLR208W	798	1.6(10)-79	Saccharomyces cerevisiae	[ui:y lr208w] [pn:protein transport protein:protein transport protein sec13] [gn:sec13:18167] [gtcf:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5059	15735377_f2_3	6212	20315	228	76	YLR208W	291	8.6(10)-26	Saccharomyces cerevisiae	[ui:y lr208w] [pn:protein transport protein:protein transport protein sec13] [gn:sec13:18167] [gtcf:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
b2x14395.y	12672062_f2_1	6213	20316	414	138	YLR262C	454	4.5(10)-43	Saccharomyces cerevisiae	[ui:y lr262c] [pn:gip-binding protein of the rab family] [gn:yp16] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5294	13084678_c1_9	6214	20317	345	115	YLR268W	198	6.2(10)-16	Saccharomyces cerevisiae	[ui:y lr268w] [pn:high copy suppressor of ypt1 null mutation:protein transport protein sec22:protein sly2] [gn:sec22:sly2:18479] [gtcf:12.6:12.10:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5294	13865676_c3_13	6215	20318	378	126	YLR268W	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:y lr268w] [pn:high copy suppressor of ypt1 null mutation:protein transport protein sec22:protein sly2] [gn:sec22:sly2:18479] [gtcf:12.6:12.10:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1382	9925053_c3_6	6216	20319	723	241	YML012W	539	4.5(10)-52	Saccharomyces cerevisiae	[ui:ym1012w] [pn:component of the copi-coated vesicles, 25 kda:hyothetical 24.1 kd protein in ppz1-sps5 intergenic region precursor] [gn:erv25:ym9571] [gtcf:12.10:12.16] [kegfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerev
CONTIG5218	4765925_c2_10	6217	20320	459	153	YML001W	123	6.7(10)-8	Saccharomyces cerevisiae	[ui:ym1001w] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt7] [gn:ypt7:vam4:ym8270] [gtcf:12.10:12.16:12.6] [kegfc:14.2] [sgdfc:8.3.0:8.7.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5771	24414062_f1_4	6218	20321	1425	475	YML287W	991	5.7(10)-100	Saccharomyces cerevisiae	[ui:ym1287w] [pn:coatomer complex gamma chain:gamma-cop of secretory pathway vesicles:coatomer gamma subunit:gamma-coat protein:gamma-cop] [gn:sec21:n0543] [gtcf:12.10:12.16] [kegfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces c

CONTIG5771	34183137_f2_17	6219	20322	1209	403	YNL287W	765	5.0(10)-76	Saccharomyces cerevisiae	[ui:ynl287w] [pn:coatomer complex gamma chain:gamma-cop of secretory pathway vesicles:coatomer gamma subunit:gamma-coat protein:gamma-cop] [gn:sec21:n0543] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces c
CONTIG4146	22837890_f2_3	6220	20323	561	187	YOR075W	152	1.8(10)-10	Saccharomyces cerevisiae	[ui:yor075w] [pn:syntaxin:t-snare of the er:protein] [gn:ufc1] [gtcf:12.10:12.15:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.4.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3096	789055_g2_3	6221	20324	513	171	YOR094W	502	3.7(10)-48	Saccharomyces cerevisiae	[ui:yor094w] [pn:adp-ribosylation factor 3] [gn:arf3.yor3172w] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4244	6750050_f3_5	6222	20325	564	188	YPL218W	682	3.2(10)-67	Saccharomyces cerevisiae	[ui:yp1218w] [pn:gip-binding protein of the arf family:gip-binding protein] [gn:sar1] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2371	20492010_f3_3	6223	20326	777	259	YPL085W	117	4.5(10)-8	Saccharomyces cerevisiae	[ui:yp1085w] [pn:multidomain vesicle coat protein] [gn:sec16] [gtcf:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0:9.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5542	24632717_c1_14	6224	20327	570	190	YPL085W	141	4.0(10)-8	Saccharomyces cerevisiae	[ui:ypi085w] [pn:multidomain vesicle coat protein] [gn:sec16] [gicfc:12.10:12.16] [keggfc:14.2] [sgdfe:6.4:0.8:3.0:9.4:0.9:9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5542	203936_c2_18	6225	20328	2640	880	YPL085W	182	2.2(10)-11	Saccharomyces cerevisiae	[ui:ypi085w] [pn:multidomain vesicle coat protein] [gn:sec16] [gicfc:12.10:12.16] [keggfc:14.2] [sgdfe:6.4:0.8:3.0:9.4:0.9:9.0] [db:gic-saccharomyces cerevisiae]
CONTIG3413	10585825_f3_3	6226	20329	354	118	YPL010W	212	2.0(10)-17	Saccharomyces cerevisiae	[ui:ypi010w] [pn:coatomer complex zeta chain:coatomer zeta subunit:zeta-coat protein:zeta-cop] [gn:rei3:ipa7w:yp8132] [gicfc:12.10:12.16] [keggfc:14.2] [sgdfe:8.3:0.9:9.0] [db:gic-saccharomyces cerevisiae]
CONTIG3413	787757_f3_4	6227	20330	264	88	YPL010W	122	7.0(10)-8	Saccharomyces cerevisiae	[ui:ypi010w] [pn:coatomer complex zeta chain:coatomer zeta subunit:zeta-coat protein:zeta-cop] [gn:rei3:ipa7w:yp8132] [gicfc:12.10:12.16] [keggfc:14.2] [sgdfe:8.3:0.9:9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4477	23648437_f3_2	6228	20331	498	166	YPR017C	146	2.0(10)-10	Saccharomyces cerevisiae	[ui:ypf017c] [pn:gdp/gtp exchange factor for sec4p:protein] [gn:dss4] [gicfc:12.10:12.16] [keggfc:14.2] [sgdfe:8.3:0.9:9.0] [db:gic-saccharomyces cerevisiae]



CONTIG3742	4766936_c1_8	6229	20332	864	288	YPR181C	759	2.2(10)-75	Saccharomyces cerevisiae	[ui:ypri81c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23;p9705] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5369	14552287_f3_5	6230	20333	1956	652	YPR181C	407	7.2(10)-98	Saccharomyces cerevisiae	[ui:ypri81c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23;p9705] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5369	20485688_f3_6	6231	20334	273	91	YPR181C	220	4.0(10)-17	Saccharomyces cerevisiae	[ui:ypri81c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23;p9705] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5745	15835192_f3_7	6232	20335	1176	392	YPR181C	1256	4.7(10)-128	Saccharomyces cerevisiae	[ui:ypri81c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23;p9705] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5811	16658452_f2_10	6233	20336	2586	862	YPR181C	395	2.7(10)-51	Saccharomyces cerevisiae	[ui:ypri81c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23;p9705] [gctc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gic-saccharomyces cerevisiae]

CONTIG4077	16798577_c1_5	6234	20337	933	311	YJR005W	203	2.2(10)-15	Saccharomyces cerevisiae	[ui:yjr005w] [pn:clathrin-associated protein complex, beta chain:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap11:yap80j1422] [gctc:12.10:12.16:12.6] [ke
CONTIG3679	4066317_c3_5	6235	20338	864	288	YJR005W	416	2.0(10)-38	Saccharomyces cerevisiae	[ui:yjr005w] [pn:clathrin-associated protein complex, beta chain:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap11:yap80j1422] [gctc:12.10:12.16:12.6] [ke
CONTIG5482	957500_c2_20	6236	20339	507	169	YJR058C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:yjr058c] [pn:clathrin-associated protein 17, small subunit:clathrin coat assembly protein ap17:clathrin coat associated protein ap17:plasma membrane adaptor ap-2 17 kd protein:ha2 17 kd subunit:clathrin assembly protein 2 small cha
CONTIG1425	11739205_f1_1	6237	20340	807	269	YKL135C	144	5.2(10)-9	Saccharomyces cerevisiae	[ui:ykl135c] [pn:beta-adaptin:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap12] [gctc:12.10:12.16:12.6] [kegct:14.2] [sgdgc:6.4.0:8.7.0:9.9.0] [db:gct-sa

CONTIG2023	23455050_f2_1	6238	20341	903	301	YKL135C	579	2.6(10)-56	Saccharomyces cerevisiae	[ui:y:kl135c] [pn:beta-adaptin:probable beta-large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap12] [gfcf:12.10:12.16:12.6] [keggfc:14.2] [sgdfc:6.4:0.8:7.0:9.9:0] [db:gfc-sa
CONTIG2771	10972806_f1_3	6239	20342	372	124	YKL135C	345	1.3(10)-30	Saccharomyces cerevisiae	[ui:y:kl135c] [pn:beta-adaptin:probable beta-large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap12] [gfcf:12.10:12.16:12.6] [keggfc:14.2] [sgdfc:6.4:0.8:7.0:9.9:0] [db:gfc-sa
CONTIG5783	14728343_f2_12	6240	20343	552	184	YLR080W	162	2.7(10)-11	Saccharomyces cerevisiae	[ui:y:lr080w] [pn:strong similarity to emp47p] [gfcf:12.10:12.16] [keggfc:14.2] [sgdfc:9.9:0] [db:gfc-saccharomyces cerevisiae]
CONTIG3030	6756938_f1_1	6241	20344	390	130	YLR170C	390	2.7(10)-36	Saccharomyces cerevisiae	[ui:y:lr170c] [pn:clathrin-associated protein:ap complex, small subunit ap19:clathrin coat assembly protein ap19:golgi adaptor ap-1 19 kd adaptin:ha1 19 kd subunit:clathrin assembly protein complex

CONTIG5548	33767162_f2_5	6242	20345	324	108	YBR132C	125	4.2(10)-7	Saccharomyces cerevisiae	[ui:ybr132c] [pn:strong similarity to amino-acid permeases:hypothetical amino-acid permease in vma2-cks1 intergenic region] [gn:ybr1007] [gtcf:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5765	20320930_f2_12	6243	20346	855	285	YBR132C	397	1.1(10)-41	Saccharomyces cerevisiae	[ui:ybr132c] [pn:strong similarity to amino-acid permeases:hypothetical amino-acid permease in vma2-cks1 intergenic region] [gn:ybr1007] [gtcf:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5765	12588156_f2_13	6244	20347	873	291	YBR132C	457	2.2(10)-43	Saccharomyces cerevisiae	[ui:ybr132c] [pn:strong similarity to amino-acid permeases:hypothetical amino-acid permease in vma2-cks1 intergenic region] [gn:ybr1007] [gtcf:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3979	4801715_c1_8	6245	20348	225	75	YDR160W	151	1.2(10)-9	Saccharomyces cerevisiae	[ui:ydr160w] [pn:similarity to amino acid permeases [yp1p and dip5p] [gtcf:12.1:12.6] [kegfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3979	4018766_c2_10	6246	20349	1341	447	YDR160W	734	9.9(10)-73	Saccharomyces cerevisiae	[ui:ydr160w] [pn:similarity to amino acid permeases lyp1p and dip5p] [gtcf:12.1:12.6] [keggtc:14.2] [sgdtc:1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3979	23921887_c3_11	6247	20350	384	128	YDR160W	127	4.2(10)-7	Saccharomyces cerevisiae	[ui:ydr160w] [pn:similarity to amino acid permeases lyp1p and dip5p] [gtcf:12.1:12.6] [keggtc:14.2] [sgdtc:1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5410	234380_c1_12	6248	20351	1191	397	YDR508C	651	6.2(10)-64	Saccharomyces cerevisiae	[ui:ydr508c] [pn:high-affinity glutamine permease] [gn:gnp1:d9719] [gtcf:12.1:12.6] [keggtc:14.2] [sgdtc:1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5787	10265628_c3_35	6249	20352	1731	577	YDR508C	1233	1.3(10)-125	Saccharomyces cerevisiae	[ui:ydr508c] [pn:high-affinity glutamine permease] [gn:gnp1:d9719] [gtcf:12.1:12.6] [keggtc:14.2] [sgdtc:1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5787	24788890_c3_33	6250	20353	1728	576	YDR508C	966	2.6(10)-97	Saccharomyces cerevisiae	[ui:ydr508c] [pn:high-affinity glutamine permease] [gn:gnp1:d9719] [gtcf:12.1:12.6] [keggtc:14.2] [sgdtc:1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2473	3938462_f2_2	6251	20354	639	213	YFL055W	306	2.2(10)-31	Saccharomyces cerevisiae	[ui:yf055w] [pn:similarity to gap1p and other amino acid permeases:hypothetical amino-acid permease in thi5-emp47 intergenic region] [gtcf:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b9x13d75.x	12353513_c3_2	6252	20355	615	205	YFL055W	571	1.8(10)-55	Saccharomyces cerevisiae	[ui:yf055w] [pn:similarity to gap1p and other amino acid permeases:hypothetical amino-acid permease in thi5-emp47 intergenic region] [gtcf:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3223	22385953_f1_1	6253	20356	1311	437	YHL036W	860	4.4(10)-86	Saccharomyces cerevisiae	[ui:yhl036w] [pn:methionine permease:hypothetical 60.6 kd protein in cbp2-ssb1 intergenic region] [gn:mup3] [gtcf:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3098	34494828_c3_4	6254	20357	1455	485	YKL174C	678	8.5(10)-67	Saccharomyces cerevisiae	[ui:ykl174c] [pn:similarity to choline transport protein hnm1p:hypothetical amino-acid permease in ste3-gin10 intergenic region] [gn:yki639] [gtcf:12.2:11.1] [keggfc:14.2] [sgdfc:1.6.5:7.4.0:7.5.0:17.0.0] [db:gtc-saccharomyces cerevi

CONTIG411	4691002_c3_2	6255	20358	525	175	YPL274W	164	2.7(10)-11	Saccharomyces cerevisiae	[ui:yp1274w] [pn:strong similarity to amino-acid transport proteins] [gtcf:12.1] [keggtc:14.2] [sgdfe:1.1.3:7.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1576	9782688_f1_1	6256	20359	765	255	YPL265W	376	2.5(10)-34	Saccharomyces cerevisiae	[ui:yp1265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcf:12.1:12.6] [keggtc:14.2] [sgdfe:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2689	13690811_c2_4	6257	20360	381	127	YPL265W	146	2.5(10)-9	Saccharomyces cerevisiae	[ui:yp1265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcf:12.1:12.6] [keggtc:14.2] [sgdfe:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3496	17205_f3_3	6258	20361	402	134	YPL265W	105	6.2(10)-5	Saccharomyces cerevisiae	[ui:yp1265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcf:12.1:12.6] [keggtc:14.2] [sgdfe:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5548	35162952_f1_4	6259	20362	1044	348	YPL265W	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:yp1265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcf:12.1:12.6] [keggtc:14.2] [sgdfe:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x11276.x	25672876_c3_1	6260	20363	564	188	YPL265W	358	2.5(10)-32	Saccharomyces cerevisiae	[ui:yp1265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcf:12.1:12.6] [keggtc:14.2] [sgdfe:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3075	32210432_c3_5	6261	20364	1143	381	YNR031C	1109	4.0(10)-112	Saccharomyces cerevisiae	[ui:ym031c] [pn:map kinase kinase of the high osmolality signal transduction pathway:serine/threonine protein kinase skk2:suppressor of sensor kinase 2] [gn:ssk2:n3276] [gctfc:12.11:12.13:1.3] [ec:2.7.-.] [kegfc:14.1] [sgdf]
CONTIG4286	2110885_f3_2	6262	20365	2619	873	YNR031C	784	7.4(10)-85	Saccharomyces cerevisiae	[ui:ym031c] [pn:map kinase kinase of the high osmolality signal transduction pathway:serine/threonine protein kinase skk2:suppressor of sensor kinase 2] [gn:ssk2:n3276] [gctfc:12.11:12.13:1.3] [ec:2.7.-.] [kegfc:14.1] [sgdf]
CONTIG5729	24411529_c2_22	6263	20366	774	258	YBL064C	644	3.3(10)-63	Saccharomyces cerevisiae	[ui:yb064c] [pn:strong similarity to thiol-specific antioxidant enzyme:hypothetical 29.5 kd protein in ubp13-kip1 intergenic region] [gn:yb0503:yb0524] [gctfc:12.12] [kegfc:14.2] [sgdf:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2019	16578517_f2_1	6264	20367	1359	453	YBR043C	663	1.5(10)-85	Saccharomyces cerevisiae	[ui:ybr043c] [pn:similarity to benomyl/methotrexate resistance protein:hypothetical 77.3 kd protein in fig1-gip1 intergenic region] [gn:ybr0413] [gctfc:12.12:12.6:13.3] [kegfc:14.2] [sgdf:7.10.0:11.3.0:17.0.0] [db:gic-saccharomyces



CONTIG5647	1990642_c2_14	6265	20368	1560	520	YBR180W	470	2.8(10)-76	Saccharomyces cerevisiae	[lui:ybr180w] [pn:similarity to drug resistance proteins:hypothetical 63.4 kd protein in smy2-rps101 intergenic region] [gn:ybr1242] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16081.y	35836703_c3_8	6266	20369	378	126	YCL069W	91	0.0027	Saccharomyces cerevisiae	[lui:ycl069w] [pn:strong similarity to drug resistance protein sge1:hypothetical 50.2 kd protein in hml 5"region] [gn:ycl69w] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3010	2131562_f2_3	6267	20370	1464	488	YCR023C	444	1.3(10)-86	Saccharomyces cerevisiae	[lui:ycr023c] [pn:member of major facilitator superfamily multidrug-resistance protein family 2:hypothetical 69.2 kd protein in hsp30-pmp1 intergenic region] [gn:ycr23c:ycr241] [gtcf:12.12:12.6] [kegfc:14.2] [sgdfe:7.11.0:11.3.0:17.0]
CONTIG4693	6760956_c3_5	6268	20371	918	306	YCR023C	546	1.7(10)-57	Saccharomyces cerevisiae	[lui:ycr023c] [pn:member of major facilitator superfamily multidrug-resistance protein family 2:hypothetical 69.2 kd protein in hsp30-pmp1 intergenic region] [gn:ycr23c:ycr241] [gtcf:12.12:12.6] [kegfc:14.2] [sgdfe:7.11.0:11.3.0:17.0]

CONTIG5644	21984453_f2_4	6269	20372	372	124	YCR023C	174	2.3(10)-12	Saccharomyces cerevisiae	[ui:ycr023c] [pn:member of major facilitator superfamily multidrug-resistance protein family 2:hyposhethical 69.2 kd protein in hsp30-pmp1 intergenic region] [gn:ycr23c:ycr241] [gtcf:12.12:12.6] [kegfc:14.2] [sgdfe:7.11.0:11.3.0:17.0]
CONTIG1849	29531277_c2_7	6270	20373	942	314	YDL100C	782	8.0(10)-78	Saccharomyces cerevisiae	[ui:ydl100c] [pn:similarity to e.coli arsenical pump-driving atpase] [gtcf:12.12] [kegfc:14.2] [sgdfe:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1433	666715_f1_1	6271	20374	849	283	YDR135C	707	1.2(10)-68	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:ycf1] [gtcf:12.6:12.12:12.13] [kegfc:14.2] [sgdfe:7.9.0:8.5.0.9:10.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4113	22475090_c2_4	6272	20375	1716	572	YDR135C	1582	9.5(10)-202	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:ycf1] [gtcf:12.6:12.12:12.13] [kegfc:14.2] [sgdfe:7.9.0:8.5.0.9:10.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4155	12537878_c1_3	6273	20376	2250	750	YDR135C	1716	8.5(10)-177	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:yctf1] [gctc:12.6:12.12:12.13] [keggfc:14.2] [sgdfe:7.9.0:8.5.0:9.10.0:1.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG397	1995832_c3_3	6274	20377	1191	397	YDR135C	408	1.0(10)-36	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:yctf1] [gctc:12.6:12.12:12.13] [keggfc:14.2] [sgdfe:7.9.0:8.5.0:9.10.0:1.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3463	13722300_c3_3	6275	20378	1464	488	YFR022W	631	5.2(10)-81	Saccharomyces cerevisiae	[ui:yfr022w] [pn:similarity to rod1 p.hypothetical 79.7 kd protein in fab1-pes4 intergenic region] [gctc:12.12] [keggfc:14.2] [sgdfe:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5613	19767203_c1_20	6276	20379	1773	591	YFR022W	231	9.0(10)-30	Saccharomyces cerevisiae	[ui:yfr022w] [pn:similarity to rod1 p.hypothetical 79.7 kd protein in fab1-pes4 intergenic region] [gctc:12.12] [keggfc:14.2] [sgdfe:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5613	23628562_c3_24	6277	20380	249	83	YFR022W	106	6.2(10)-5	Saccharomyces cerevisiae	[ui:yfr022w] [pn:similarity to rod1 p.hypothetical 79.7 kd protein in fab1-pes4 intergenic region] [gctc:12.12] [keggfc:14.2] [sgdfe:11.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG5814	24400437_c3_50	6278	20381	705	235	YGL016W	257	7.5(10)-21	Saccharomyces cerevisiae	[ui:yg1016w] [pn:pleiotropic drug resistance regulatory protein:pleiotropic drug resistance regulatory protein 6] [gn:pdrt6] [gtcf:12.12] [keggfc:14.2] [sgdfe:11.3.0] [db:gtc-saccharomyces cerevisiae]
b2x11126.x	6833390_c1_4	6279	20382	441	147	YGL016W	135	7.9(10)-8	Saccharomyces cerevisiae	[ui:yg1016w] [pn:pleiotropic drug resistance regulatory protein:pleiotropic drug resistance regulatory protein 6] [gn:pdrt6] [gtcf:12.12] [keggfc:14.2] [sgdfe:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4203	13101687_c1_5	6280	20383	774	258	YGR138C	782	8.0(10)-78	Saccharomyces cerevisiae	[ui:yr138c] [pn:similarity to multidrug resistance proteins:hypothetical 67.6 kd protein in pas5-cb12 intergenic region] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4751	5961700_c2_10	6281	20384	936	312	YGR138C	369	1.6(10)-33	Saccharomyces cerevisiae	[ui:yr138c] [pn:similarity to multidrug resistance proteins:hypothetical 67.6 kd protein in pas5-cb12 intergenic region] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3322	894762_f1_1	6282	20385	939	313	YGR197C	362	4.4(10)-33	Saccharomyces cerevisiae	[ui: ygr197c] [pn: involved in nitroguanidine resistance: nitrosoguanidine resistance protein sng1] [gn: sng1: g7591] [gtcf: 1.2.12.6: 13.3] [keggfc: 14.2] [sgdfc: 7.10.0: 11.3.0: 17.0.0] [db: gtc-saccharomyces cerevisiae]
CONTIG4771	11837837_c2_9	6283	20386	525	175	YGR197C	159	8.4(10)-11	Saccharomyces cerevisiae	[ui: ygr197c] [pn: involved in nitroguanidine resistance: nitrosoguanidine resistance protein sng1] [gn: sng1: g7591] [gtcf: 1.2.12.6: 13.3] [keggfc: 14.2] [sgdfc: 7.10.0: 11.3.0: 17.0.0] [db: gtc-saccharomyces cerevisiae]
CONTIG4771	2616401_c1_6	6284	20387	270	90	YGR197C	107	3.2(10)-5	Saccharomyces cerevisiae	[ui: ygr197c] [pn: involved in nitroguanidine resistance: nitrosoguanidine resistance protein sng1] [gn: sng1: g7591] [gtcf: 1.2.12.6: 13.3] [keggfc: 14.2] [sgdfc: 7.10.0: 11.3.0: 17.0.0] [db: gtc-saccharomyces cerevisiae]

CONTIG635	14191067_ft_1	6285	20388	702	234	YGR197C	348	1.8(10)-31	Saccharomyces cerevisiae	[ui:Ygr197c] [pn:involved in nitroguanidine resistance:nitrosoguanidine resistance:protein sng1] [gn:sgl:g7591] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1618	7837_ft_1	6286	20389	1074	358	YGR224W	380	9.4(10)-35	Saccharomyces cerevisiae	[ui:Ygr224w] [pn:strong similarity to drug resistance protein sge1:hypothetical 67.2 kd protein in pet54-die2 intergenic region] [gn:g8537] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerev
CONTIG66	11113175_ft_1	6287	20390	630	210	YGR224W	308	8.0(10)-27	Saccharomyces cerevisiae	[ui:Ygr224w] [pn:strong similarity to drug resistance protein sge1:hypothetical 67.2 kd protein in pet54-die2 intergenic region] [gn:g8537] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerev
CONTIG906	901928_ft_1	6288	20391	540	180	YGR224W	146	2.5(10)-9	Saccharomyces cerevisiae	[ui:Ygr224w] [pn:strong similarity to drug resistance protein sge1:hypothetical 67.2 kd protein in pet54-die2 intergenic region] [gn:g8537] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerev

CONTIG1647	31926000_c2_4	6289	20392	1014	338	YHL040C	693	2.2(10)-68	Saccharomyces cerevisiae	[ui:yh040c] [pn:similarity to c.carbonum toxin pump:hypothetical 70.9 kd protein in cbp2 5"region] [gtfc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2318	16853432_ft_1	6290	20393	426	142	YHL040C	92	0.027	Saccharomyces cerevisiae	[ui:yh040c] [pn:similarity to c.carbonum toxin pump:hypothetical 70.9 kd protein in cbp2 5"region] [gtfc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3837	4954407_c2_7	6291	20394	378	126	YHL040C	223	1.3(10)-17	Saccharomyces cerevisiae	[ui:yh040c] [pn:similarity to c.carbonum toxin pump:hypothetical 70.9 kd protein in cbp2 5"region] [gtfc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3105	25658443_c3_9	6292	20395	1494	498	YHR032W	855	1.5(10)-85	Saccharomyces cerevisiae	[ui:yh032w] [pn:ethionine resistance protein:hypothetical 64.2 kd protein in slt2-put2 intergenic region] [gn:etc1] [gtfc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3187	578126_f2_3	6293	20396	1074	358	YHR032W	497	3.0(10)-56	Saccharomyces cerevisiae	[ui:Yhr032w] [pn:ethionine resistance protein:hyposphthalic 64.2 kd protein in sIt2-put2 intergenic region] [gn:erc1] [gctc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:1.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3200	4175067_f1_1	6294	20397	720	240	YHR032W	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:Yhr032w] [pn:ethionine resistance protein:hyposphthalic 64.2 kd protein in sIt2-put2 intergenic region] [gn:erc1] [gctc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:1.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3246	4379637_c3_2	6295	20398	1023	341	YHR032W	600	1.6(10)-58	Saccharomyces cerevisiae	[ui:Yhr032w] [pn:ethionine resistance protein:hyposphthalic 64.2 kd protein in sIt2-put2 intergenic region] [gn:erc1] [gctc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:1.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3342	2347062_c3_23	6296	20399	1452	484	YHR032W	750	2.0(10)-74	Saccharomyces cerevisiae	[ui:Yhr032w] [pn:ethionine resistance protein:hyposphthalic 64.2 kd protein in sIt2-put2 intergenic region] [gn:erc1] [gctc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:1.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]



CONTIG5707	21601512_f3_13	6297	20400	1593	531	YHR048W	1073	1.2(10)-108	Saccharomyces cerevisiae	[ui:yhr048w] [pn:similarity to multidrug resistance proteins:hypothetical 57.8 kd protein in aap1-smf2 intergenic region] [gctc:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:1.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4670	1464556_c3_10	6298	20401	372	124	YJR015W	186	9.0(10)-14	Saccharomyces cerevisiae	[ui:yjr015w] [pn:strong similarity to sng1p:hypothetical 58.1 kd protein in spc1-ilv3 intergenic region] [gn:j1448] [gctc:12.12] [kegfc:14.2] [sgdfe:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4865	12526586_f3_7	6299	20402	1188	396	YJR015W	224	5.9(10)-16	Saccharomyces cerevisiae	[ui:yjr015w] [pn:strong similarity to sng1p:hypothetical 58.1 kd protein in spc1-ilv3 intergenic region] [gn:j1448] [gctc:12.12] [kegfc:14.2] [sgdfe:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2879	5985002_f2_1	6300	20403	291	97	YJR104C	315	2.5(10)-28	Saccharomyces cerevisiae	[ui:yjr104c] [pn:copper-zinc superoxide dismutase:superoxide dismutase:cu-zn] [gn:sod1:j1968] [gctc:12.12:14.1] [ec:1.15.1.1] [kegfc:14.1] [sgdfe:9.2.0:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3171	12687761_f2_1	6301	20404	480	160	YJR104C	554	1.2(10)-53	Saccharomyces cerevisiae	[ui:yjr104c] [pn:copper-zinc superoxide dismutase:superoxide dismutase:cu-zn] [gn:sod1:j1968] [gctc:12.12:14.1] [ec:1.15.1.1] [kegfc:14.1] [sgdfe:9.2.0:11.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG5673	25015_f3_17	6302	20405	2445	815	YKL064W	964	2.2(10)-135	Saccharomyces cerevisiae	[ui:yk1064w] [pn:overexpression overcomes manganese toxicity:hypothetical 109.7 kd protein in nup100-msn4 intergenic region] [gn:mmr2] [gtcf:12.12:12.6] [keggfc:14.2] [sgdfc:1.8.1:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2972	5906632_c3_1	6303	20406	1455	485	YKL004W	314	1.7(10)-32	Saccharomyces cerevisiae	[ui:yk1004w] [pn:aureobasidin-resistance protein:hypothetical 45.2 kd protein tp114a-mrp17 intergenic region] [gn:aur1] [gtcf:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5664	5947586_c3_23	6304	20407	1902	634	YKR105C	361	2.8(10)-61	Saccharomyces cerevisiae	[ui:ykr105c] [pn:strong similarity to sge1p and hypothetical protein ycl069w:hypothetical 63.4 kd protein in sir1 3"region] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2718	13929502_f2_2	6305	20408	1323	441	YLL028W	486	1.8(10)-46	Saccharomyces cerevisiae	[ui:yll028w] [pn:similarity to multidrug resistance proteins] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4898	5111008_c3_7	6306	20409	1266	422	YLL028W	988	1.2(10)-99	Saccharomyces cerevisiae	[ui:yll028w] [pn:similarity to multidrug resistance proteins] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]



CONTIG5744	21750300_f1_1	6313	20416	627	209	YML028W	766	4.0(10)-76	Saccharomyces cerevisiae	[ui:ym1028w] [pn:thiol-specific antioxidant:thiol-specific antioxidant protein:pp] [gn:tsa1:tsa] [gtcf:12.12] [kegfc:14.2] [sgdfc:9.2.0:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG763	34017686_c1_2	6314	20417	252	84	YNL259C	147	1.6(10)-10	Saccharomyces cerevisiae	[ui:yn1259c] [pn:antioxidant protein and metal homeostasis factor:metal homeostasis factor atx1] [gn:atx1:n0840] [gtcf:12.12:12.6] [kegfc:14.2] [sgdfc:1.8.1:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4821	14537702_c1_10	6315	20418	1515	505	YNL065W	750	2.0(10)-74	Saccharomyces cerevisiae	[ui:yn1065w] [pn:similarity to resistance proteins:hypothetical 65.3 kd protein in sun4-mas5 intergenic region] [gn:n2417:yn12417w] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5691	24414132_f1_1	6316	20419	1194	398	YNL065W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yn1065w] [pn:similarity to resistance proteins:hypothetical 65.3 kd protein in sun4-mas5 intergenic region] [gn:n2417:yn12417w] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG2305	12673131_c2_4	6317	20420	360	120	YNR055C	120	1.5(10)-6	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:hol1 protein] [gn:hol1:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2809	31400_c1_6	6318	20421	798	266	YNR055C	161	5.9(10)-15	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:hol1 protein] [gn:hol1:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2809	23640702_c1_5	6319	20422	615	205	YNR055C	208	4.9(10)-16	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:hol1 protein] [gn:hol1:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5052	11726562_c2_4	6320	20423	1788	596	YNR055C	1514	2.2(10)-155	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:hol1 protein] [gn:hol1:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5216	502290_f3_8	6321	20424	1353	451	YNR055C	730	2.6(10)-72	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:holl protein] [gn:holl:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5307	24254561_f3_6	6322	20425	1329	443	YNR055C	177	1.2(10)-20	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:holl protein] [gn:holl:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5307	3947553_f2_3	6323	20426	438	146	YNR055C	143	4.9(10)-9	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:holl protein] [gn:holl:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5644	35369200_c3_20	6324	20427	795	265	YNR055C	248	2.2(10)-20	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:holl protein] [gn:holl:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5644	1370781_c1_14	6325	20428	1197	399	YNR055C	222	1.2(10)-15	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:holl protein] [gn:holl:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG8	24234561_c1_1	6326	20429	249	83	YNR055C	94	0.00089	Saccharomyces cerevisiae	[ui:ym055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:holl protein] [gn:holl:n3494] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1524	16042580_f2_1	6327	20430	507	169	YOL130W	312	6.7(10)-27	Saccharomyces cerevisiae	[ui:yol130w] [pn:aluminium resistance protein] [gn:alr1] [gtcf:12.12] [kegfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3482	4720302_f1_1	6328	20431	2358	786	YOL130W	1002	3.8(10)-101	Saccharomyces cerevisiae	[ui:yol130w] [pn:aluminium resistance protein] [gn:alr1] [gtcf:12.12] [kegfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4240	20337552_c2_2	6329	20432	927	309	YOR273C	255	5.2(10)-21	Saccharomyces cerevisiae	[ui:yor273c] [pn:similarity to resistance proteins] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5024	34178918_f2_1	6330	20433	1083	361	YOR273C	719	3.7(10)-71	Saccharomyces cerevisiae	[ui:yor273c] [pn:similarity to resistance protein] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3194	35832152_f1_1	6331	20434	1191	397	YOR378W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yor378w] [pn:strong similarity to aminotriazole resistance protein] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3610	3994386_c1_7	6332	20435	426	142	YOR378W	127	2.1(10)-7	Saccharomyces cerevisiae	[ui:yor378w] [pn:strong similarity to aminotriazole resistance protein] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4609	14645400_f1_1	6333	20436	1650	550	YOR378W	963	5.2(10)-97	Saccharomyces cerevisiae	[ui:yor378w] [pn:strong similarity to aminotriazole resistance protein] [gtcf:12.12:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4928	2908412_f3_4	6334	20437	1554	518	YPL092W	285	4.5(10)-43	Saccharomyces cerevisiae	[ui:yp1092w] [pn:sulfite sensitivity protein:sulfite sensitivity protein ssu1] [gn:ssu1:pg16w] [gtcf:12.12] [kegfc:14.2] [sgdfe:11.3.0] [db:gtc-saccharomyces cerevisiae]



CONTIG4203	5328252_c3_7	6335	20438	948	316	YPR156C	673	1.5(10)-85	Saccharomyces cerevisiae	[ui:yp156c] [pn:similarity to multidrug resistance proteins] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5501	12111067_f2_8	6336	20439	1788	596	YPR156C	795	3.3(10)-79	Saccharomyces cerevisiae	[ui:yp156c] [pn:similarity to multidrug resistance proteins] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5501	4569426_f1_5	6337	20440	1173	391	YPR156C	355	6.0(10)-32	Saccharomyces cerevisiae	[ui:yp156c] [pn:similarity to multidrug resistance proteins] [gtcf:12.12:12.6:13.3] [keggfc:14.2] [sgdfe:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4433	23728188_f3_4	6338	20441	582	194	YBL061C	467	3.6(10)-44	Saccharomyces cerevisiae	[ui:ybl061c] [pn:protoplast regeneration and killer toxin resistance protein:skt5 protein] [gn:skt5:ybl0506:ybl0519] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1471	860932_f3_4	6339	20442	555	185	YCR002C	95	0.00119	Saccharomyces cerevisiae	[ui:ycr002c] [pn:cell division control protein 10] [gn:cdc10:ycr2c:ycr022] [gtcf:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfe:1.5.2:3.0:3.8:0.3:9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4404	14625325_c2_8	6340	20443	1122	374	YCR002C	1147	1.7(10)-116	Saccharomyces cerevisiae	[ui:ycr002c] [pn:cell division control protein 10] [gn:cdc10:ycr02c:ycr022] [gicfc:12.13:12.16:12.8:12.9] [kegfc:14.2] [sgdfe:1.5:2.3:0.3:8:0.3:9:0:9:3:0] [db:gic-saccharomyces cerevisiae]
CONTIG2588	14100915_c3_4	6341	20444	687	229	YCR010C	262	1.0(10)-22	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5:2] [db:gic-saccharomyces cerevisiae]
CONTIG2588	10603428_c1_3	6342	20445	408	136	YCR010C	203	1.8(10)-16	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5:2] [db:gic-saccharomyces cerevisiae]
CONTIG2876	20491558_f2_3	6343	20446	330	110	YCR010C	168	1.5(10)-12	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5:2] [db:gic-saccharomyces cerevisiae]

CONTIG2876	4718926_f3_4	6344	20447	192	64	YCR010C	95	0.00024	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs16l-adj1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]
CONTIG2876	4722625_f1_2	6345	20448	528	176	YCR010C	207	6.9(10)-17	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs16l-adj1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]
CONTIG2978	4041535_c2_7	6346	20449	927	309	YCR010C	585	6.0(10)-57	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs16l-adj1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]
CONTIG3805	800962_f2_3	6347	20450	735	245	YCR010C	477	1.7(10)-45	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs16l-adj1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]
CONTIG450	20110302_c2_3	6348	20451	948	316	YCR010C	682	3.2(10)-67	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs16l-adj1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]

CONTIG5652	33407503_f3_15	6349	20452	963	321	YCR010C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34;hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]
CONTIG1471	2362586_f2_3	6350	20453	279	93	YDL225W	106	4.2(10)-5	Saccharomyces cerevisiae	[ui:ydl225w] [pn:similarity to cdc11p, cdc3p and human cdc10 protein] [gicfc:12.13:12.8:12.9] [kegfc:14.2] [sgdfe:1.5.2:3.2.0:3.3.0:3.8:0:3.9.0] [db:gic-saccharomyces cerevisiae]
b1x13266.y	24016950_f1_1	6351	20454	558	186	YDL225W	283	3.1(10)-24	Saccharomyces cerevisiae	[ui:ydl225w] [pn:similarity to cdc11p, cdc3p and human cdc10 protein] [gicfc:12.13:12.8:12.9] [kegfc:14.2] [sgdfe:1.5.2:3.2.0:3.3.0:3.8:0:3.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4815	10833337_f3_4	6352	20455	1611	537	YDL203C	146	6.7(10)-7	Saccharomyces cerevisiae	[ui:ydl203c] [pn:similarity to skt5p] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]
CONTIG5450	22681442_g3_13	6353	20456	840	280	YDR277C	142	2.2(10)-7	Saccharomyces cerevisiae	[ui:ydr277c] [pn:repressor of hexose transport genes:mth1 protein] [gn:mth1.d9954] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gic-saccharomyces cerevisiae]

CONTIG5694	24511453_c2_19	6354	20457	2121	707	YGR070W	136	3.2(10)-5	Saccharomyces cerevisiae	[ui:Ygr070w] [pn:trt1 expression protein for rho1p:rho1 gdp-gtp exchange protein 1:protein kinase c suppressor skc1] [gn:rom1:skc1] [gtcf:12.13:12.8] [keggfc:13.3] [sgdfe:1.5.2:3.2:0.10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG1831	6928402_f1_1	6355	20458	336	112	YGR227W	144	9.5(10)-17	Saccharomyces cerevisiae	[ui:Ygr227w] [pn:trt1 expression promoting protein:die2 protein] [gn:die2:g8547] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4081	14254677_f2_1	6356	20459	786	262	YGR227W	160	2.0(10)-24	Saccharomyces cerevisiae	[ui:Ygr227w] [pn:trt1 expression promoting protein:die2 protein] [gn:die2:g8547] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5556	29944799_c1_13	6357	20460	945	315	YHR107C	942	9.0(10)-95	Saccharomyces cerevisiae	[ui:Yhr107c] [pn:cell division control protein 12:septin] [gn:cdcl2:clal0:psl7] [gtcf:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfe:1.5.2:3.2:0.3:3.0:3.8:0.3:9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2842	6814032_f3_1	6358	20461	858	286	YHR155W	102	5.0(10)-5	Saccharomyces cerevisiae	[ui:Yhr155w] [pn:strong similarity to snf1p-interacting protein sip3:p-hypothetical 143.6 kd protein in spo16-rec104 intergenic region] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5775	9850261_f3_17	6359	20462	1416	472	YJL033C	711	4,5(10)-84	Saccharomyces cerevisiae	[ui:yjl033c] [pn:camp dependent protein kinase, regulatory subunit:camp-dependent protein kinase regulatory chain] [gn:regl:beyl:sral] [gtcf:12.13:12.15:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.4.0:9.2.0:11.1.0:15.0.0] [db:gtc-saccharomyce
CONTIG2906	24022187_f3_3	6360	20463	1263	421	YJR076C	697	8,1(10)-69	Saccharomyces cerevisiae	[ui:yjr076c] [pn:septin:cell division control protein 11] [gn:cdcl1:psl9:j1833] [gtcf:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.0:3.8.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5020	26835776_c3_11	6361	20464	1440	480	YJR076C	298	1,6(10)-26	Saccharomyces cerevisiae	[ui:yjr076c] [pn:septin:cell division control protein 11] [gn:cdcl1:psl9:j1833] [gtcf:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.0:3.8.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2553	4695257_c2_1	6362	20465	780	260	YJR090C	100	0.032	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grt1 protein] [gn:grt1:col2:ca80:j1885] [gtcf:12.13:12.2:12.8:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.1.0:3.2.0:8.7.0:11.1.0] [db:gtc-saccharomyces cer

CONTIG3400	33673152_f3_3	6363	20466	1281	427	YJR090C	719	2.0(10)-70	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:col2:ca80:j1885] [gtcf:12.13:12.2:12.8:13.2] [kegfc:14.2] [sgdfc:1.5.2:3.1.0.3.2.0.8.7.0:11.1.0] [db:gtc-saccharomyces cer]
CONTIG3779	10631500_c1_6	6364	20467	807	269	YJR090C	279	3.7(10)-23	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:col2:ca80:j1885] [gtcf:12.13:12.2:12.8:13.2] [kegfc:14.2] [sgdfc:1.5.2:3.1.0.3.2.0.8.7.0:11.1.0] [db:gtc-saccharomyces cer]
CONTIG3784	159563_c2_4	6365	20468	1458	486	YJR090C	167	6.7(10)-9	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:col2:ca80:j1885] [gtcf:12.13:12.2:12.8:13.2] [kegfc:14.2] [sgdfc:1.5.2:3.1.0.3.2.0.8.7.0:11.1.0] [db:gtc-saccharomyces cer]
CONTIG4576	14725937_f1_3	6366	20469	444	148	YLR150W	105	1.7(10)-5	Saccharomyces cerevisiae	[ui:ylr150w] [pn:specific affinity for guanine-rich quadruplex nucleic acids:suppressor protein mpt4:stm1 protein:gu4 nucleic-binding protein 2:g4p2 protein] [gn:mpt4:stm1:sto1:19634] [gtcf:12.13] [kegfc:14.2] [sgdfc:1.5.2] [db:gtc-

CONTIG3241	14625928_f2_1	6367	20470	1431	477	YLR330W	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ylr330w] [pn:chitin synthesis protein] [gn:chs5] [gicfc:1.4:7.2] [kegfc:14.2] [sgdfe:1.5.2:3.2:0.3:3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3811	4063801_f2_1	6368	20471	1665	555	YLR371W	313	1.1(10)-26	Saccharomyces cerevisiae	[ui:ylr371w] [pn:gdp/gip exchange factor for rho1p:rho1 gdp-gip exchange protein 2] [gn:rom2:8039] [gicfc:12.13:12.8] [kegfc:14.2] [sgdfe:1.5.2:3.2:0.10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5358	13750326_c1_8	6369	20472	2046	682	YLR371W	1006	1.5(10)-101	Saccharomyces cerevisiae	[ui:ylr371w] [pn:gdp/gip exchange factor for rho1p:rho1 gdp-gip exchange protein 2] [gn:rom2:8039] [gicfc:12.13:12.8] [kegfc:14.2] [sgdfe:1.5.2:3.2:0.10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5358	25587508_c3_13	6370	20473	549	183	YLR371W	342	9.1(10)-30	Saccharomyces cerevisiae	[ui:ylr371w] [pn:gdp/gip exchange factor for rho1p:rho1 gdp-gip exchange protein 2] [gn:rom2:8039] [gicfc:12.13:12.8] [kegfc:14.2] [sgdfe:1.5.2:3.2:0.10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5795	24335958_c2_34	6371	20474	420	140	YML048W	94	0.00054	Saccharomyces cerevisiae	[ui:ym1048w] [pn:involved in glucose repression] [gn:eff2] [gicfc:12.13] [kegfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]



b2x10461.y	21898302_f3_1	6372	20475	696	232	YML048W	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:ym1048w] [pn:involved in glucose repression] [gn:eft2] [gctc:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2086	6737932_c1_2	6373	20476	1110	370	YNL257C	398	8.1(10)-36	Saccharomyces cerevisiae	[ui:yn1257c] [pn:snf1p protein kinase interacting protein:sip3 protein] [gn:sip3:n0844] [gctc:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
b3x17312.x	213252_f1_1	6374	20477	729	243	YNL257C	215	2.7(10)-16	Saccharomyces cerevisiae	[ui:yn1257c] [pn:snf1p protein kinase interacting protein:sip3 protein] [gn:sip3:n0844] [gctc:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2147	24414068_c1_2	6375	20478	447	149	YNL201C	308	1.8(10)-26	Saccharomyces cerevisiae	[ui:yn1201c] [pn:involved in regulation of carbon metabolism:hypothetical 98.1 kd protein in spx19-gcr2 intergenic region] [gn:1366] [gctc:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3791	25594427_f1_1	6376	20479	1212	404	YNL201C	170	3.6(10)-19	Saccharomyces cerevisiae	[ui:yn1201c] [pn:involved in regulation of carbon metabolism:hypothetical 98.1 kd protein in spx19-gcr2 intergenic region] [gn:1366] [gctc:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:gtc-saccharomyces cerevisiae]

63x15662.y	7260150_fl_1	6377	20480	528	176	YNL201C	283	8.6(10)-24	Saccharomyces cerevisiae	[ui:ynl201c] [pn:involved in regulation of carbon metabolism:hypothetical 98.1 kd protein in spx19-ger2 intergenic region] [gn:l366] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:glc-saccharomyces cerevisiae]
CONTIG5747	10756952_c2_40	6378	20481	564	188	YNL090W	621	9.3(10)-61	Saccharomyces cerevisiae	[ui:ynl090w] [pn:gip-binding protein of the rho subfamily of ras-like proteins:rho2 protein] [gn:rho2:n2237] [gtcf:12.13:12.16:12.8] [keggfc:14.2] [sgdfe:1.5.2:3.2.0:9.4.0:10.2.3] [db:glc-saccharomyces cerevisiae]
CONTIG1952	14187550_f2_2	6379	20482	207	69	YNR002C	130	3.1(10)-8	Saccharomyces cerevisiae	[ui:ynr002c] [pn:strong similarity to y.lipolytica glyoxylate pathway regulator gpr1:fun34 protein] [gn:fun34:n2029] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:glc-saccharomyces cerevisiae]
CONTIG3471	6413176_c1_5	6380	20483	876	292	YNR002C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:ynr002c] [pn:strong similarity to y.lipolytica glyoxylate pathway regulator gpr1:fun34 protein] [gn:fun34:n2029] [gtcf:12.13] [keggfc:14.2] [sgdfe:1.5.2] [db:glc-saccharomyces cerevisiae]

CONTIG598	14570462_c2_4	6381	20484	768	256	YNR002C	535	1.2(10)-51	Saccharomyces cerevisiae	[ui:ynr002c] [pn:strong similarity to y_lipolytica glyoxylate pathway regulator gpt1:fun34 protein] [gn:fun34:n2029] [gtcf:12.13] [kegfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1152	1250000_f3_4	6382	20485	843	281	YOR125C	691	3.6(10)-68	Saccharomyces cerevisiae	[ui:yor125c] [pn:involved in glucose repression:cat5 protein:ubiquinone biosynthesis protein coq7] [gn:cat5:coq7:n3284:yor3284c] [gtcf:12.13:9.12] [kegfc:14.2] [sgdfc:1.5.2:1.7.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4461	6924017_c2_4	6383	20486	1734	578	YPL026C	259	4.0(10)-42	Saccharomyces cerevisiae	[ui:yp1026c] [pn:suppressor kinase of snf3] [gn:sk31] [gtcf:12.13] [kegfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3974	1956881_c2_3	6384	20487	858	286	YPL002C	299	1.3(10)-38	Saccharomyces cerevisiae	[ui:yp1002c] [pn:involved in glucose derepression] [gn:snf8] [gtcf:12.13] [kegfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4717	34156676_f1_1	6385	20488	606	202	YPR165W	548	5.0(10)-53	Saccharomyces cerevisiae	[ui:yp165w] [pn:gtp-binding protein of the rho subfamily of ras-like proteins:rho1 protein] [gn:rho1:p9325] [gtcf:12.13:12.16:12.8] [kegfc:13.3] [sgdfc:1.5.2:3.2.0:9.4.0:10.2.3] [db:gtc-saccharomyces cerevisiae]

CONTIG4819	4723132_f1_1	6386	20489	606	202	YPR165W	737	4.7(10)-73	Saccharomyces cerevisiae	[ui:yp165w] [pn:gip-binding protein of the rho subfamily of ras-like proteins:rho1 protein] [gn:rho1:p9325] [gtcf:12.13:12.16:12.8] [keggfc:13.3] [sgdfe:1.5.2:3.2.0:9.4.0:10.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4082	11022577_f2_1	6387	20490	1239	413	YHL003C	1089	2.3(10)-110	Saccharomyces cerevisiae	[ui:yhl003c] [pn:longevity-assurance protein 1] [gn:lag1] [gtcf:12.13:12.8] [keggfc:14.2] [sgdfe:3.10.0:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3085	34413175_c2_5	6388	20491	1263	421	YIL123W	1009	7.0(10)-102	Saccharomyces cerevisiae	[ui:yil123w] [pn:strong similarity to sun4p, uth1p, nea3p and c.wickertamii beta-glucosidase:hyothetical 48.1 kd protein in kgd1-rpil intergenic region] [gtcf:12.13] [keggfc:14.2] [sgdfe:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4489	14459376_f1_2	6389	20492	534	178	YIL123W	235	3.5(10)-19	Saccharomyces cerevisiae	[ui:yil123w] [pn:strong similarity to sun4p, uth1p, nea3p and c.wickertamii beta-glucosidase:hyothetical 48.1 kd protein in kgd1-rpil intergenic region] [gtcf:12.13] [keggfc:14.2] [sgdfe:11.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2528	395426_f3_1	6390	20493	1302	434	YKL008C	336	1.5(10)-30	Saccharomyces cerevisiae	[ui:ykl008c] [pn:strong similarity to lag1p:hypothetical 49.0 kd protein utd4-cap1 intergenic region] [gn:ykl156] [gtcf:12.13] [kegfc:14.2] [sgdfc:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5207	10198557_f2_3	6391	20494	984	328	YDL025C	329	4.2(10)-29	Saccharomyces cerevisiae	[ui:ydl025c] [pn:ser/thr protein kinase of the dead/death box family] [gtcf:12.13:13.2] [kegfc:14.2] [sgdfc:11.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	20345001_c2_28	6392	20495	2706	902	YDR466W	755	2.2(10)-78	Saccharomyces cerevisiae	[ui:ydr466w] [pn:similarity ser/thr protein kinase] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4588	4959626_c3_8	6393	20496	810	270	YDR490C	113	0.00084	Saccharomyces cerevisiae	[ui:ydr490c] [pn:similarity to ser/thr protein kinases] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1369	3914057_c3_4	6394	20497	1080	360	YDR507C	1088	3.0(10)-110	Saccharomyces cerevisiae	[ui:ydr507c] [pn:ser/thr-protein kinase] [gn:gin4] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1896	31688383_f1_1	6395	20498	1575	525	YDR507C	177	1.2(10)-20	Saccharomyces cerevisiae	[ui:ydr507c] [pn:ser/thr-protein kinase] [gn:gin4] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2418	13930402_c3_4	6396	20499	951	317	YDR507C	207	1.8(10)-15	Saccharomyces cerevisiae	[lui:ydr507c] [pn:ser/thr-protein kinase] [gn:gin4] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfe:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1440	23600192_f2_1	6397	20500	771	257	YFR014C	308	1.3(10)-27	Saccharomyces cerevisiae	[lui:yfr014c] [pn:ca2+/calmodulin-dependent ser/thr protein kinase type i:calcium/calmodulin-dependent protein kinase type i] [gn:cnk1] [gtcf:12.13:12.8:14.1] [ec:2.7.1.123] [keggfc:14.1] [sgdfe:3.1.0:9.2.0:15.0.0] [db:gtc-saccharomyc]
CONTIG4006	14540907_f1_2	6398	20501	687	229	YGR080W	153	1.3(10)-10	Saccharomyces cerevisiae	[lui:ygr080w] [pn:weak similarity to human tyrosine kinase a6:hypothetical 37.1 kd protein in pac10-tom20 intergenic region] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfe:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4006	22363752_f3_4	6399	20502	573	191	YGR080W	148	4.9(10)-10	Saccharomyces cerevisiae	[lui:ygr080w] [pn:weak similarity to human tyrosine kinase a6:hypothetical 37.1 kd protein in pac10-tom20 intergenic region] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfe:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4652	23859655_c3_8	6400	20503	909	303	YGR262C	336	1.5(10)-30	Saccharomyces cerevisiae	[lui:ygr262c] [pn:weak similarity to protein kinases:hypothetical 29.9 kd protein in apl6-mes1 intergenic region] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfe:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5520	4093775_f1_3	6401	20504	1263	421	YHR205W	248	1.0(10)-18	Saccharomyces cerevisiae	[ui:yhr205w] [pn:strong similarity to s.pombe sock1 protein kinase:camp-dependent protein kinase sch9] [gn:sch9:kom1] [gctc:12.13:12.8] [ec:2.7.1.37] [kegfc:14.1] [sgdfe:3.8.0:15.0.0] [db:gctc-saccharomyces cerevisiae]
CONTIG5520	23539062_f1_4	6402	20505	1131	377	YHR205W	1351	4.0(10)-138	Saccharomyces cerevisiae	[ui:yhr205w] [pn:strong similarity to s.pombe sock1 protein kinase:camp-dependent protein kinase sch9] [gn:sch9:kom1] [gctc:12.13:12.8] [ec:2.7.1.37] [kegfc:14.1] [sgdfe:3.8.0:15.0.0] [db:gctc-saccharomyces cerevisiae]
CONTIG5619	29782012_c3_20	6403	20506	4140	1380	YJL095W	1086	1.7(10)-137	Saccharomyces cerevisiae	[ui:yjl095w] [pn:ser/thr protein kinase of the mek family:serine/threonine protein kinase bck1/slk/ssp31] [gn:bck1:slk:ssp31:ias3:j0906] [gctc:12.13:12.8:13.2:14.1] [ec:2.7.-.-] [kegfc:14.1] [sgdfe:3.1.0.3.2.0.3.8.0.9.2.0:10.2.5]
CONTIG5276	23832527_c1_11	6404	20507	972	324	YLR063W	489	9.0(10)-47	Saccharomyces cerevisiae	[ui:yhr063w] [pn:ser/thr protein kinase] [gctc:12.13:14.3] [kegfc:14.2] [sgdfe:15.0.0:13.0.0] [db:gctc-saccharomyces cerevisiae]
CONTIG1192	433325_f2_1	6405	20508	519	173	YMR216C	281	1.1(10)-23	Saccharomyces cerevisiae	[ui:ymr216c] [pn:similarity to ser/thr protein kinases] [gctc:12.13:14.3] [kegfc:14.2] [sgdfe:15.0.0:13.0.0] [db:gctc-saccharomyces cerevisiae]

CONTIG4234	6837841_f2_1	6406	20509	1731	577	YMR216C	688	4.5(10)-107	Saccharomyces cerevisiae	[ui:ymr216c] [pn:similarity to ser/thr protein kinases] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16065.y	12632160_c1_5	6407	20510	186	62	YMR216C	119	2.5(10)-6	Saccharomyces cerevisiae	[ui:ymr216c] [pn:similarity to ser/thr protein kinases] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3370	22866412_c1_6	6408	20511	2367	789	YOL100W	545	1.1(10)-51	Saccharomyces cerevisiae	[ui:yol100w] [pn:similarity to ser/thr protein kinases] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3118	1178827_c1_1	6409	20512	846	282	YOL045W	938	2.3(10)-94	Saccharomyces cerevisiae	[ui:yol045w] [pn:similarity to ser/thr protein kinase] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4637	15819388_f2_1	6410	20513	2799	933	YOL045W	334	2.3(10)-62	Saccharomyces cerevisiae	[ui:yol045w] [pn:similarity to ser/thr protein kinase] [gtcf:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1179	547030_f3_1	6411	20514	1086	362	YOL016C	1065	8.3(10)-108	Saccharomyces cerevisiae	[ui:yol016c] [pn:ca2+/calmodulin-dependent ser/thr protein kinase, type ii:calcium/calmodulin-dependent protein kinase type ii] [gn:cmk2] [gtcf:12.13:14.1] [ec:2.7.1.123] [keggfc:14.1] [sgdfc:9.2.0:15.0.0] [db:gtc-saccharomyces cerv]



CONTIG2469	20343800_f2_1	6412	20515	1458	486	YOR267C	587	3.7(10)-57	Saccharomyces cerevisiae	[ui:yor267c] [pn:similarity to ser/thr protein kinases] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3562	11797027_f3_4	6413	20516	1401	467	YOR267C	869	4.9(10)-87	Saccharomyces cerevisiae	[ui:yor267c] [pn:similarity to ser/thr protein kinases] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG2806	10161442_f2_1	6414	20517	858	286	YPL236C	233	1.7(10)-19	Saccharomyces cerevisiae	[ui:yp1236c] [pn:similarity to s.pombe hypothetical protein spac3h1.13] [gtcf:12.13:14.1] [kegfc:14.2] [sgdfc:15.0:13.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5023	4070138_c2_9	6415	20518	1317	439	YPL203W	1355	1.5(10)-138	Saccharomyces cerevisiae	[ui:yp1203w] [pn:camp-dependent protein kinase 2, catalytic chain:camp-dependent protein kinase type 2:pka 2] [gn:ipk2:ykr1:pkaz] [gtcf:12.13:12.8] [ec:2.7.1.37] [kegfc:13.1] [sgdfc:9.2.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5056	488131_f1_4	6416	20519	1212	404	YPL203W	1302	6.4(10)-133	Saccharomyces cerevisiae	[ui:yp1203w] [pn:camp-dependent protein kinase 2, catalytic chain:camp-dependent protein kinase type 2:pka 2] [gn:ipk2:ykr1:pkaz] [gtcf:12.13:12.8] [ec:2.7.1.37] [kegfc:13.1] [sgdfc:9.2.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5114	192076_f1_1	6417	20520	2856	952	YPL150W	695	1.3(10)-68	Saccharomyces cerevisiae	[ui:yp1150w] [pn:similarity to ser/thr kinases] [gtcf:12.13:14.3] [kegfc:14.2] [sgdfc:15.0:13.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG728	25976513_c2_2	6418	20521	546	182	YPL141C	486	1.2(10)-45	Saccharomyces cerevisiae	[ui:yp1141c] [pn:strong similarity to protein kinase kin4p] [gicfc:12.13:14.3] [keggfc:14.2] [sgdfe:15.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5628	863912_f3_8	6419	20522	2574	858	YAL041W	853	7.0(10)-98	Saccharomyces cerevisiae	[ui:yal041w] [pn:gtp/gdp exchange factor for cdc42p:cell division control protein 24:calcium regulatory protein] [gn:cdc24:cls4] [gicfc:12.13:12.8:12.9] [keggfc:13.1:13.3] [sgdfe:3.2.0:3.0:3.8.0:9.2.0:10.1.3:10.2.4] [db:gic-saccharo
CONTIG4077	25835202_c3_7	6420	20523	408	136	YDL135C	158	1.1(10)-11	Saccharomyces cerevisiae	[ui:ydl135c] [pn:rho gdp dissociation inhibitor with activity toward rho1p] [gn:rdi1] [gicfc:12.13:12.8] [keggfc:14.2] [sgdfe:3.2.0:10.2.4] [db:gic-saccharomyces cerevisiae]
CONTIG4319	5273502_c1_8	6421	20524	621	207	YDL135C	515	1.6(10)-49	Saccharomyces cerevisiae	[ui:ydl135c] [pn:rho gdp dissociation inhibitor with activity toward rho1p] [gn:rdi1] [gicfc:12.13:12.8] [keggfc:14.2] [sgdfe:3.2.0:10.2.4] [db:gic-saccharomyces cerevisiae]
CONTIG5749	24665635_c2_23	6422	20525	600	200	YDL135C	113	4.2(10)-5	Saccharomyces cerevisiae	[ui:ydl135c] [pn:rho gdp dissociation inhibitor with activity toward rho1p] [gn:rdi1] [gicfc:12.13:12.8] [keggfc:14.2] [sgdfe:3.2.0:10.2.4] [db:gic-saccharomyces cerevisiae]

CONTIG2879	34573406_c1_3	6423	20526	915	305	YPL115C	295	7.0(10)-25	Saccharomyces cerevisiae	[ui:yp1115c] [pn:gpase-activating protein for cdc42p and rho1p:protein] [gn:bem3] [gtcf:12.13:12.8:12.9] [keggfc:13.3] [sgdfc:3.2.0:3.0:9.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG3171	23626442_c1_4	6424	20527	825	275	YPL115C	295	7.0(10)-25	Saccharomyces cerevisiae	[ui:yp1115c] [pn:gpase-activating protein for cdc42p and rho1p:protein] [gn:bem3] [gtcf:12.13:12.8:12.9] [keggfc:13.3] [sgdfc:3.2.0:3.0:9.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
b9x10d83.y	29329385_c2_1	6425	20528	453	151	YPL115C	111	3.0(10)-5	Saccharomyces cerevisiae	[ui:yp1115c] [pn:gpase-activating protein for cdc42p and rho1p:protein] [gn:bem3] [gtcf:12.13:12.8:12.9] [keggfc:13.3] [sgdfc:3.2.0:3.0:9.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	4296926_f1_6	6426	20529	564	188	YBR109C	470	9.3(10)-45	Saccharomyces cerevisiae	[ui:ybr109c] [pn:calmodulin] [gn:cmd1:ybr0904] [gtcf:12.13:12.16:12.6:12.8:12.9] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.3.0:3.8.0:8.7.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]

CONTIG4093	19695760_c2_5	6427	20530	924	308	YBR200W	271	1.8(10)-29	Saccharomyces cerevisiae	[ui:ybr200w] [pn:bud emergence mediator:bem1 protein] [gn:bem1:sro1:ybr1412] [gtcf:12.13:12.16:12.8:12.9] [kegfc:13.1] [sgdfc:3.2.0:3.3.0:3.8.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG4093	23478436_c2_4	6428	20531	978	326	YBR200W	370	5.4(10)-34	Saccharomyces cerevisiae	[ui:ybr200w] [pn:bud emergence mediator:bem1 protein] [gn:bem1:sro1:ybr1412] [gtcf:12.13:12.16:12.8:12.9] [kegfc:13.1] [sgdfc:3.2.0:3.3.0:3.8.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG2864	26386562_c1_5	6429	20532	1113	371	YBR200W	153	2.7(10)-8	Saccharomyces cerevisiae	[ui:ybr200w] [pn:bud emergence mediator:bem1 protein] [gn:bem1:sro1:ybr1412] [gtcf:12.13:12.16:12.8:12.9] [kegfc:13.1] [sgdfc:3.2.0:3.3.0:3.8.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG2881	25410625_c3_8	6430	20533	465	155	YOR149C	100	0.0015	Saccharomyces cerevisiae	[ui:yor149c] [pn:protein kinase c pathway protein:protein] [gn:snp3] [gtcf:12.13:12.8] [kegfc:14.2] [sgdfc:3.1.0:3.2.0:3.8.0:10.2.7] [db:gtc-saccharomyces cerevisiae]

CONTIG2881	4334458_c2_7	6431	20534	582	194	YOR149C	232	9.4(10)-19	Saccharomyces cerevisiae	[ui:yor149c] [pn:protein kinase c pathway protein:protein] [gn:smp3] [gctc:12.13:12.8] [keggfc:14.2] [sgdfe:3.1.0:3.2.0:3.8.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG1696	3994012_fl_1	6432	20535	810	270	YPL106C	927	3.5(10)-93	Saccharomyces cerevisiae	[ui:yp1106c] [pn:heat shock protein of hsp70 family:heat shock protein homolog ssc1] [gn:ssc1:ms3:hp3c] [gctc:12.7:13.2] [keggfc:14.2] [sgdfe:10.2.7:10.4.8:11.1.0] [db:gtc-saccharomyces cerevisiae]
b2x11950.y	34617300_c1_1	6433	20536	510	170	YDL128W	354	1.8(10)-32	Saccharomyces cerevisiae	[ui:ydl128w] [pn:ca2+-transport:h+/ca2+ exchange protein, vacuolar] [gn:vcx1] [gctc:12.5:12.13:12.16] [keggfc:14.2] [sgdfe:1.8.2:7.2.8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2355	2740682_c1_3	6434	20537	1365	455	YGL006W	699	3.3(10)-68	Saccharomyces cerevisiae	[ui:ygl006w] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 2:vacuolar ca2+-atpase] [gn:pcal:pmc1] [gctc:12.5:12.13:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:1.8.2:7.2.7.8.0:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3119	35392812_f2_1	6435	20538	1350	450	YGL006W	574	9.1(10)-79	Saccharomyces cerevisiae	[ui:yg 006w] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 2:vacuolar ca2+-atpase] [gn:pca1:pnc1] [gtcf:12.5:12.13:12.16] [ec:3.6.1.38] [keggtc:14.1] [sgdtc:1.8.2:7.2:7.8:0.8:5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3371	9922150_c2_6	6436	20539	225	75	YPL234C	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:yp 234c] [pn:h+-atpase v0 domain 17 kd subunit, vacuolar:proteolipid protein vma11] [gn:vma1:tfp3:cls9:p1064] [gtcf:12.13:12.16:12.5:12.6] [keggtc:14.2] [sgdtc:1.8.2:6.4:0.7.2.7.8:0.8:5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5387	21490702_f3_13	6437	20540	1380	460	YPL066W	126	6.0(10)-5	Saccharomyces cerevisiae	[ui:yp 066w] [pn:involved in vacuolar traffic] [gn:yps28] [gtcf:12.13] [keggtc:14.2] [sgdtc:8.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4730	14641882_c1_9	6438	20541	1344	448	YPR173C	1338	1.1(10)-163	Saccharomyces cerevisiae	[ui:yp 173c] [pn:vacuolar sorting protein:end13 protein] [gn:end13:yps4:grd13:p9705] [gtcf:12.13:12.16] [keggtc:14.2] [sgdtc:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

b3x13880.x	32628752_f1_1	6439	20542	264	88	YJR069C	192	2.7(10)-15	Saccharomyces cerevisiae	[ui:yji069c] [pn:controls 6-n-hydroxylaminopurine sensitivity and mutagenesis:ham1 protein] [gn:ham1:j1811] [gctc:12.14] [kegfc:14.2] [sgdfe:11.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4456	9960763_c3_8	6440	20543	789	263	YKL110C	432	1.0(10)-53	Saccharomyces cerevisiae	[ui:ykl110c] [pn:involved in resistance to k.lactis killer toxin:kti12 protein] [gn:kti12:ykl500:ykl446] [gctc:12.14] [kegfc:14.2] [sgdfe:11.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5797	23628301_f3_12	6441	20544	1695	565	YAL009W	384	1.2(10)-35	Saccharomyces cerevisiae	[ui:yal009w] [pn:meiotic protein:sporulation protein] [gn:spo7] [gctc:12.15:12.8] [kegfc:14.2] [sgdfe:3.4.0:3.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5531	39038_f2_13	6442	20545	747	249	YBR057C	128	5.0(10)-6	Saccharomyces cerevisiae	[ui:ybr057c] [pn:meiotic protein:hyphothetical 41.4 kd protein in prp6-ubp14 intergenic region] [gn:mum2:ybr0514] [gctc:12.15:12.8] [kegfc:14.2] [sgdfe:3.4.0:3.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1924	23560953_c3_4	6443	20546	297	99	YCL048W	168	6.5(10)-12	Saccharomyces cerevisiae	[ui:ycl048w] [pn:strong similarity to sporulation-specific protein sps2p:hyphothetical sps2-like 52.0 kd protein in apa1/dtp-pdi1 intergenic region] [gn:ycl48w] [gctc:12.15:12.8] [kegfc:14.2] [sgdfe:3.4.0:3.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG499	24406692_f3_1	6444	20547	603	201	YCL048W	342	3.3(10)-31	Saccharomyces cerevisiae	[ui:ycl048w] [pn:strong similarity to sporulation-specific protein sps2p;hypothetical sps2-like 52.0 kd protein in apal/dtp-pd1 intergenic region] [gn:ycl48w]
										[gtcf:12.15:12.8] [kegfc:14.2] [sgdfe:3.4:0.3:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4150	30757692_f2_2	6445	20548	1542	514	YDL240W	341	1.1(10)-28	Saccharomyces cerevisiae	[ui:ydl240w] [pn:gipase-activating protein of the rho/rac family:protein] [gn:lrg1] [gtcf:12.15] [kegfc:14.2] [sgdfe:3.4:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4150	23910752_f3_6	6446	20549	1164	388	YDL240W	580	8.6(10)-63	Saccharomyces cerevisiae	[ui:ydl240w] [pn:gipase-activating protein of the rho/rac family:protein] [gn:lrg1] [gtcf:12.15] [kegfc:14.2] [sgdfe:3.4:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4150	187761_f2_3	6447	20550	411	137	YDL240W	92	0.0028	Saccharomyces cerevisiae	[ui:ydl240w] [pn:gipase-activating protein of the rho/rac family:protein] [gn:lrg1] [gtcf:12.15] [kegfc:14.2] [sgdfe:3.4:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4282	10212586_f2_2	6448	20551	903	301	YDR055W	362	2.6(10)-33	Saccharomyces cerevisiae	[ui:ydr055w] [pn:strong similarity to sps2 protein] [gtcf:12.15:12.8] [kegfc:14.2] [sgdfe:3.4:0.3:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5756	13835750_f3_11	6449	20552	1239	413	YDR055W	399	3.1(10)-37	Saccharomyces cerevisiae	[ui:ydr055w] [pn:strong similarity to sps2 protein] [gtcf:12.15:12.8] [kegfc:14.2] [sgdfe:3.4:0.3:5.0] [db:gtc-saccharomyces cerevisiae]



CONTIG2124	29879577_c3_3	6450	20553	1431	477	YDR108W	178	5.4(10)-19	Saccharomyces cerevisiae	[ui:ydr108w] [pn:sporulation specific protein:sporulation protein] [gn:gsg1] [gtcf:12.15:12.8] [kegfc:14.2] [sgdfe:3.4.0:3.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1087	1048281_f1_1	6451	20554	504	168	YDR218C	215	3.8(10)-17	Saccharomyces cerevisiae	[ui:ydr218c] [pn:septin-related sporulation protein] [gn:spr28] [gtcf:12.15:12.16:12.8] [kegfc:14.2] [sgdfe:3.4.0:3.5.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5162	1953125_c2_7	6452	20555	1557	519	YDR403W	918	3.1(10)-92	Saccharomyces cerevisiae	[ui:ydr403w] [pn:spore wall maturation protein:dtt1] [gn:dtt1:d9509] [gtcf:12.15] [kegfc:14.2] [sgdfe:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5776	4472215_f1_4	6453	20556	1140	380	YGR059W	473	4.5(10)-45	Saccharomyces cerevisiae	[ui:ygr059w] [pn:sporulation-specific septin] [gn:spr3] [gtcf:12.15:12.16] [kegfc:14.2] [sgdfe:3.4.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2552	34064625_f3_2	6454	20557	627	209	YKL165C	464	3.5(10)-43	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtcf:12.15] [kegfc:14.2] [sgdfe:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG2552	976502_f3_3	6455	20558	270	90	YKL165C	213	3.0(10)-16	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtcf:12.15] [kegfc:14.2] [sgdfe:3.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG2870	839555_c3_2	6456	20559	852	284	YKL165C	404	1.0(10)-36	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtrfc:12.15] [keggfc:14.2] [sgdgc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5472	9953437_f2_4	6457	20560	1722	574	YKL165C	1240	2.3(10)-126	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtrfc:12.15] [keggfc:14.2] [sgdgc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3459	6281875_f2_2	6458	20561	1311	437	YML115C	126	5.5(10)-5	Saccharomyces cerevisiae	[ui:yml115c] [pn:vanadate resistance protein] [gn:van1.vrg7:ym8339] [gtrfc:12.15:12.8] [keggfc:14.2] [sgdgc:3.4.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5090	550678_c3_10	6459	20562	318	106	YML115C	399	3.1(10)-37	Saccharomyces cerevisiae	[ui:yml115c] [pn:vanadate resistance protein] [gn:van1.vrg7:ym8339] [gtrfc:12.15:12.8] [keggfc:14.2] [sgdgc:3.4.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4018	6723775_f1_1	6460	20563	933	311	YML110C	934	6.2(10)-94	Saccharomyces cerevisiae	[ui:yml110c] [pn:dbf2 interacting protein:hypothetical 34.7 kd protein in ctk3-zds2 intergenic region] [gn:dbi56:ym8339] [gtrfc:12.15] [keggfc:14.2] [sgdgc:3.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2174	1285131_f1_1	6461	20564	780	260	YMR063W	119	2.3(10)-5	Saccharomyces cerevisiae	[ui:ymr063w] [pn:regulator for sporulation and invasive growth] [gn:rim9] [gicfc:12.15:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3791	9798180_f1_2	6462	20565	471	157	YNL202W	319	9.4(10)-29	Saccharomyces cerevisiae	[ui:ynl202w] [pn:sporulation-specific protein:sporulation protein spx19] [gn:spx19:n1362] [gicfc:12.15:12.6:12.8] [keggfc:14.2] [sgdfe:3.4.0:3.5.0:9.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3945	9922137_c3_5	6463	20566	936	312	YNL202W	926	4.5(10)-93	Saccharomyces cerevisiae	[ui:ynl202w] [pn:sporulation-specific protein:sporulation protein spx19] [gn:spx19:n1362] [gicfc:12.15:12.6:12.8] [keggfc:14.2] [sgdfe:3.4.0:3.5.0:9.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5353	12929652_c3_15	6464	20567	879	293	YNL202W	881	2.6(10)-88	Saccharomyces cerevisiae	[ui:ynl202w] [pn:sporulation-specific protein:sporulation protein spx19] [gn:spx19:n1362] [gicfc:12.15:12.6:12.8] [keggfc:14.2] [sgdfe:3.4.0:3.5.0:9.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG5787	10548250_c3_37	6465	20568	954	318	YOR313C	167	4.0(10)-12	Saccharomyces cerevisiae	[ui:yor313c] [pn:sporulation-specific protein:sporation-specific protein 4] [gn:spst4:o6120] [gctc:12.15] [keggfc:14.2] [sgdfe:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG1919	24391380_f2_3	6466	20569	1167	389	YAL047C	114	0.0014	Saccharomyces cerevisiae	[ui:yal047c] [pn:stu2p interactant:hypothetical 72.1 kd protein in acsl-gcv3 intergenic region] [gn:sp16:fun42] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4316	10625306_c3_9	6467	20570	705	235	YAL047C	96	0.041	Saccharomyces cerevisiae	[ui:yal047c] [pn:stu2p interactant:hypothetical 72.1 kd protein in acsl-gcv3 intergenic region] [gn:sp16:fun42] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG713	2222013_c2_3	6468	20571	429	143	YAL020C	201	5.4(10)-16	Saccharomyces cerevisiae	[ui:yal020c] [pn:alpha-tubulin suppressor:ats1 protein:alpha-tubulin suppressor 1] [gn:ats1:yal006:fun28] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
b9x13524.x	24319792_c2_6	6469	20572	318	106	YAL020C	109	9.3(10)-6	Saccharomyces cerevisiae	[ui:yal020c] [pn:alpha-tubulin suppressor:ats1 protein:alpha-tubulin suppressor 1] [gn:ats1:yal006:fun28] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG4778	36456301_c3_8	6470	20573	3078	1026	YBL034C	212	5.4(10)-13	Saccharomyces cerevisiae	[ui:yb1034c] [pn:mitotic spindle protein:mitotic spindle protein stu1] [gn:stu1:yb10416] [gtcf:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4097	32675441_f1_1	6471	20574	2652	884	YBL007C	617	1.3(10)-115	Saccharomyces cerevisiae	[ui:yb1007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:yb10321] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3731	21660187_c1_12	6472	20575	1113	371	YBL007C	99	0.078	Saccharomyces cerevisiae	[ui:yb1007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:yb10321] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b1x16816.x	110301_c3_2	6473	20576	345	115	YBL007C	279	4.2(10)-23	Saccharomyces cerevisiae	[ui:yb1007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:yb10321] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5011	10833254_c2_9	6474	20577	822	274	YBL007C	124	1.2(10)-7	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for assembly control protein:cytoskeleton control protein sla1] [gn:sla1:yb0321] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2549	3181267_c3_5	6475	20578	1257	419	YBR130C	94	0.11	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:shc3:ybr1005] [gtcf:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4178	14881552_f2_5	6476	20579	309	103	YBR130C	123	4.2(10)-7	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:shc3:ybr1005] [gtcf:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4178	24391051_f3_7	6477	20580	1152	384	YBR130C	96	0.055	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:shc3:ybr1005] [gtcf:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5321	2345083_c1_21	6478	20581	1482	494	YBR130C	103	0.017	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho: hypothetical 47.4 kd protein in vma2-dks1 intergenic region] [gn:shc3:ybr1005] [gctc:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2094	26682963_f1_1	6479	20582	1284	428	YBR172C	101	0.03599	Saccharomyces cerevisiae	[ui:ybr172c] [pn:kinesin-related protein:smy2 protein] [gn:smy2:ybr123] [gctc:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5571	35957706_f3_16	6480	20583	1920	640	YBR172C	221	7.7(10)-15	Saccharomyces cerevisiae	[ui:ybr172c] [pn:kinesin-related protein:smy2 protein] [gn:smy2:ybr123] [gctc:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2508	20426386_f2_1	6481	20584	1071	357	YCR009C	218	1.5(10)-33	Saccharomyces cerevisiae	[ui:ycr009c] [pn:similarity to human amphiphysin and rvs167p:reduced viability upon starvation protein 161] [gn:rvs161:spe161:ycr9c] [gctc:12.16:12.6:12.8] [kegfc:14.2] [sgdfc:3.2.0:8.7.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4424	13010953_f3_4	6482	20585	1395	465	YCR088W	136	2.7(10)-15	Saccharomyces cerevisiae	[ui:ycr088w] [pn:actin-binding protein:actin binding protein] [gn:abp1:ycr88w] [gctc:12.16:12.8] [kegfc:14.2] [sgdfc:3.1.0:3.2.0:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG5731	21879562_f2_10	6483	20586	363	121	YCR088W	226	5.7(10)-18	Saccharomyces cerevisiae	[ui:ycr088w] [pn:actin-binding protein:actin binding protein] [gn:abp1:ycr88w] [gdcf:12.16:12.8] [keggfc:14.2] [sgdcf:3.1.0:3.2.0:9.3.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5733	2773275_f2_8	6484	20587	876	292	YCR088W	119	0.00011	Saccharomyces cerevisiae	[ui:ycr088w] [pn:actin-binding protein:actin binding protein] [gn:abp1:ycr88w] [gdcf:12.16:12.8] [keggfc:14.2] [sgdcf:3.1.0:3.2.0:9.3.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5061	15628377_c3_13	6485	20588	837	279	YDL178W	646	2.1(10)-63	Saccharomyces cerevisiae	[ui:ydl178w] [pn:actin-interacting protein 2] [gn:alp2] [gdcf:12.16] [keggfc:14.2] [sgdcf:9.3.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5541	34100078_c3_21	6486	20589	393	131	YDL178W	284	2.1(10)-24	Saccharomyces cerevisiae	[ui:ydl178w] [pn:actin-interacting protein 2] [gn:alp2] [gdcf:12.16] [keggfc:14.2] [sgdcf:9.3.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5587	30272567_f2_5	6487	20590	816	272	YDR085C	96	0.069	Saccharomyces cerevisiae	[ui:ydr085c] [pn:involved in morphogenesis of the mating projection:atr1 protein] [gn:atr1:d4471] [gdcf:12.16:12.8:12.9] [keggfc:14.2] [sgdcf:3.2.0:3.3.0:9.3.0] [db-gtc-saccharomyces cerevisiae]



CONTIG1278	25390933_f3_3	6488	20591	555	185	YDR388W	127	1.8(10)-7	Saccharomyces cerevisiae	[ui:yd388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167.d9509] [gicfc:12.16:12.8] [kegfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4621	10040878_c2_5	6489	20592	1068	356	YDR388W	129	1.8(10)-5	Saccharomyces cerevisiae	[ui:yd388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167.d9509] [gicfc:12.16:12.8] [kegfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5180	24398876_c3_15	6490	20593	1440	480	YDR388W	1148	1.3(10)-116	Saccharomyces cerevisiae	[ui:yd388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167.d9509] [gicfc:12.16:12.8] [kegfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gic-saccharomyces cerevisiae]
b9x10802.x	188410_f2_1	6491	20594	210	70	YDR388W	122	6.7(10)-7	Saccharomyces cerevisiae	[ui:yd388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167.d9509] [gicfc:12.16:12.8] [kegfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG3405	6350826_f2_3	6492	20595	1020	340	YDR389W	290	1.3(10)-32	Saccharomyces cerevisiae	[ui:ydr389w] [pn:suppressor of actin mutation:protein] [gn:sac7] [gtcf:12.16] [keggfc:14.2] [sgdfe:6.4.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3884	10192052_f1_1	6493	20596	849	283	YDR389W	147	4.9(10)-8	Saccharomyces cerevisiae	[ui:ydr389w] [pn:suppressor of actin mutation:protein] [gn:sac7] [gtcf:12.16] [keggfc:14.2] [sgdfe:6.4.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5417	503288_c3_20	6494	20597	684	228	YDR484W	137	7.4(10)-7	Saccharomyces cerevisiae	[ui:ydr484w] [pn:suppressor of actin mutation:protein] [gn:sac2] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG725	10032590_c1_4	6495	20598	903	301	YER007W	188	1.7(10)-12	Saccharomyces cerevisiae	[ui:yer007w] [pn:required in the absence of cin8p:protein] [gn:pac2] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2273	2910900_c2_7	6496	20599	975	325	YER016W	371	1.8(10)-40	Saccharomyces cerevisiae	[ui:yer016w] [pn:binding to microtubules:hyposphinctical 38.4 kd protein in faa2-afg3 intergenic region] [gn:bin1] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3189	21883561_f3_2	6497	20600	960	320	YFL037W	1371	3.1(10)-140	Saccharomyces cerevisiae	[ui:yfl037w] [pn:beta-tubulin:tubulin beta chain] [gn:tub2] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.5.0:3.8.0:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG1599	19956502_c2_3	6498	20601	1101	367	YGL216W	397	4.0(10)-36	Saccharomyces cerevisiae	[ui:ygl216w] [pn:similarity to mouse kinesin-related protein kit3:putative kinesin-like protein ygl216w] [gicf:12.16] [keggf:14.2] [sgdfc:8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3758	23630067_f1_1	6499	20602	2148	716	YGL216W	477	8.0(10)-45	Saccharomyces cerevisiae	[ui:ygl216w] [pn:similarity to mouse kinesin-related protein kit3:putative kinesin-like protein ygl216w] [gicf:12.16] [keggf:14.2] [sgdfc:8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5733	9766885_f1_2	6500	20603	987	329	YGL116W	142	5.2(10)-7	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gicf:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5733	2241512_f2_7	6501	20604	609	203	YGL116W	228	3.7(10)-18	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gicf:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG585	1191505_f1_1	6502	20605	1053	351	YGL116W	632	6.4(10)-62	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gicf:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0:9.3.0] [db:gic-saccharomyces cerevisiae]

b9x13f58.x	960191_c2_1	6503	20606	492	164	YGL116W	151	7.2(10)-10	Saccharomyces cerevisiae	[ui:yg116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gicfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5814	25445930_f2_9	6504	20607	1242	414	YGL003C	472	7.0(10)-55	Saccharomyces cerevisiae	[ui:yg1003c] [pn:similarity to cdc20p and human p55cdc:hypothetical trp-asp repeats containing protein in pmc1-tfg2 intergenic region] [gicfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5814	5275063_f1_1	6505	20608	588	196	YGL003C	595	5.2(10)-58	Saccharomyces cerevisiae	[ui:yg1003c] [pn:similarity to cdc20p and human p55cdc:hypothetical trp-asp repeats containing protein in pmc1-tfg2 intergenic region] [gicfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5521	23539626_c1_24	6506	20609	546	182	YGR078C	452	7.5(10)-43	Saccharomyces cerevisiae	[ui:yg078c] [pn:required in the absence of cin8p:protein] [gn:pac10] [gicfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4045	13866715_c3_10	6507	20610	834	278	YHR023W	94	0.28	Saccharomyces cerevisiae	[ui:ynr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gicfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG4494	4773286_f2_3	6508	20611	1419	473	YHR023W	129	0.00018	Saccharomyces cerevisiae	[ui:Yhr023w] [pn:Type II myosin heavy chain:myosin-1 isoform:Type II myosin] [gn:myo1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4627	978506_c2_3	6509	20612	2592	864	YHR023W	1731	2.2(10)-178	Saccharomyces cerevisiae	[ui:Yhr023w] [pn:Type II myosin heavy chain:myosin-1 isoform:Type II myosin] [gn:myo1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5325	12673188_f2_4	6510	20613	2169	723	YHR023W	228	6.0(10)-18	Saccharomyces cerevisiae	[ui:Yhr023w] [pn:Type II myosin heavy chain:myosin-1 isoform:Type II myosin] [gn:myo1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5335	20391000_f3_5	6511	20614	1884	628	YHR023W	135	6.0(10)-5	Saccharomyces cerevisiae	[ui:Yhr023w] [pn:Type II myosin heavy chain:myosin-1 isoform:Type II myosin] [gn:myo1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]
b9x13n32.x	11767285_f3_1	6512	20615	492	164	YHR023W	93	0.05299	Saccharomyces cerevisiae	[ui:Yhr023w] [pn:Type II myosin heavy chain:myosin-1 isoform:Type II myosin] [gn:myo1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG3220	10656511_c3_6	6513	20616	648	216	YJL034C	556	7.2(10)-54	Saccharomyces cerevisiae	[lui:yjl034c] [pn:f-actin capping protein, beta subunit:f-actin capping protein beta subunit] [gn:cap2] [gtcf:12.16:12.8:12.9] [kegfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4003	12538962_f1_1	6514	20617	1941	647	YJL042W	529	4.0(10)-53	Saccharomyces cerevisiae	[lui:yjl042w] [pn:microtubule-associated protein:map-homologous protein 1] [gn:mhp1:j1206] [gtcf:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5634	2116682_f2_7	6515	20618	2085	695	YJL042W	469	5.7(10)-42	Saccharomyces cerevisiae	[lui:yjl042w] [pn:microtubule-associated protein:map-homologous protein 1] [gn:mhp1:j1206] [gtcf:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5230	3906252_c1_15	6516	20619	1095	365	YJR065C	1112	2.5(10)-125	Saccharomyces cerevisiae	[lui:yjr065c] [pn:actin related protein:actin-like protein act4] [gn:arp3:act4:j1760] [gtcf:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1877	308_f3_6	6517	20620	606	202	YJR134C	110	2.2(10)-5	Saccharomyces cerevisiae	[lui:yjr134c] [pn:similarity to paramyosin, myosin:hypothetical 81.2 kd protein in nmd5-hom6 intergenic region] [gn:j2120] [gtcf:12.16] [kegfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4822	11837806_c2_13	6518	20621	564	188	YJR134C	96	0.029	Saccharomyces cerevisiae	[ui:yjr134c] [pn:similarity to paramyosin, myosin:hypothetical 81.2 kd protein in nm5-hom6 intergenic region] [gn:j2120] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2827	15801_c2_5	6519	20622	636	212	YKL179C	391	9.8(10)-36	Saccharomyces cerevisiae	[ui:ykl179c] [pn:similarity to nufl:p:hypothetical 77.5 kd protein in prp1-ste3 intergenic region] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x11927.x	22776681_f3_2	6520	20623	411	137	YKL179C	176	1.8(10)-12	Saccharomyces cerevisiae	[ui:ykl179c] [pn:similarity to nufl:p:hypothetical 77.5 kd protein in prp1-ste3 intergenic region] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5295	33407052_f1_1	6521	20624	1017	339	YKL079W	107	0.00579	Saccharomyces cerevisiae	[ui:ykl079w] [pn:kinesin-related protein:kinesin-related protein smy1:suppressor protein smy1] [gn:smy1:ykl409] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b2x17273.x	13959792_f3_1	6522	20625	525	175	YKL079W	192	3.2(10)-14	Saccharomyces cerevisiae	[ui:ykl079w] [pn:kinesin-related protein:kinesin-related protein smy1:suppressor protein smy1] [gn:smy1:ykl409] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4510	1257680_c2_3	6523	20626	771	257	YKL007W	321	5.7(10)-29	Saccharomyces cerevisiae	[lui:ykl007w] [pn:f-actin capping protein alpha subunit] [gn:cap1:ykl155] [gicf:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4813	10984801_f1_3	6524	20627	441	147	YLL050C	552	1.8(10)-53	Saccharomyces cerevisiae	[lui:yll050c] [pn:cofilin, actin binding and severing protein:cofilin] [gn:cof1] [gicf:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5622	1173287_c3_18	6525	20628	2949	983	YLL021W	521	6.5(10)-54	Saccharomyces cerevisiae	[lui:yll021w] [pn:involved in cell polarity:spa2 protein] [gn:spa2:pea1:11209] [gicf:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5622	4084632_c2_16	6526	20629	1515	505	YLL021W	339	7.2(10)-34	Saccharomyces cerevisiae	[lui:yll021w] [pn:involved in cell polarity:spa2 protein] [gn:spa2:pea1:11209] [gicf:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG1715	1259628_c3_9	6527	20630	183	61	YLL001W	214	1.8(10)-16	Saccharomyces cerevisiae	[lui:yll001w] [pn:dynamitin-related protein:dynamitin-related protein dnm1] [gn:dnm1:11381] [gicf:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.3.0] [db:gic-saccharomyces cerevisiae]



CONTIG3452	23613381_f1_1	6528	20631	498	166	YLL001W	466	9.3(10)-44	Saccharomyces cerevisiae	[ui:y l001w] [pn:dynamitin-related protein:dynamitin-related protein dnm1] [gn:dnm1:11381] [gctc:12.16:12.6] [keggfc:14.2] [sgdfe:8.7.0:9.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG3452	26345338_f1_2	6529	20632	807	269	YLL001W	327	1.2(10)-28	Saccharomyces cerevisiae	[ui:y l001w] [pn:dynamitin-related protein:dynamitin-related protein dnm1] [gn:dnm1:11381] [gctc:12.16:12.6] [keggfc:14.2] [sgdfe:8.7.0:9.3.0] [db:glc-saccharomyces cerevisiae]
b9x11d54.y	1196938_c1_2	6530	20633	762	254	YLL001W	814	3.2(10)-81	Saccharomyces cerevisiae	[ui:y l001w] [pn:dynamitin-related protein:dynamitin-related protein dnm1] [gn:dnm1:11381] [gctc:12.16:12.6] [keggfc:14.2] [sgdfe:8.7.0:9.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG2156	24256265_c1_3	6531	20634	951	317	YLR045C	208	2.7(10)-29	Saccharomyces cerevisiae	[ui:y lr045c] [pn:suppressor of a cs tubulin mutation:suppressor of tubulin stu2] [gn:stu2:12108] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:glc-saccharomyces cerevisiae]
CONTIG3576	2907812_c2_6	6532	20635	1164	388	YLR085C	314	5.9(10)-51	Saccharomyces cerevisiae	[ui:y lr085c] [pn:actin-related protein] [gn:arp6] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:glc-saccharomyces cerevisiae]

CONTIG4625	4197192_c3_8	6533	20636	333	111	YLR314C	284	1.8(10)-24	Saccharomyces cerevisiae	[ui:ylr314c] [pn:cell division control protein:cell division control protein 3] [gn:cdc3:18543] [gctc:12.16:12.8:12.9] [keggtc:14.2] [sgdgc:3.2.0:3.3.0:3.8.0:3.9.0:3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2878	473526_c3_5	6534	20637	1230	410	YLR319C	244	2.0(10)-49	Saccharomyces cerevisiae	[ui:ylr319c] [pn:bud site selection protein:bud site selection protein bud6:actin interacting protein 3] [gn:bud6:ai3:18543] [gctc:12.16:12.8] [keggtc:14.2] [sgdgc:3.2.0:3.0] [db:gic-saccharomyces cerevisiae]
CONTIG949	4183150_c1_5	6535	20638	732	244	YLR319C	439	1.0(10)-40	Saccharomyces cerevisiae	[ui:ylr319c] [pn:bud site selection protein:bud site selection protein bud6:actin interacting protein 3] [gn:bud6:ai3:18543] [gctc:12.16:12.8] [keggtc:14.2] [sgdgc:3.2.0:3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4214	22037713_f2_4	6536	20639	855	285	YLR337W	170	1.0(10)-11	Saccharomyces cerevisiae	[ui:ylr337w] [pn:verprolin] [gn:vrp1] [gctc:12.16:12.6:12.8] [keggtc:14.2] [sgdgc:3.1.0:3.2.0:8.7.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5761	898500_f3_16	6537	20640	294	98	YLR337W	125	6.5(10)-7	Saccharomyces cerevisiae	[ui:ylr337w] [pn:verprolin] [gn:vrp1] [gctc:12.16:12.6:12.8] [keggtc:14.2] [sgdgc:3.1.0:3.2.0:8.7.0:9.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG5403	34642778_f1_2	6538	20641	1950	650	YLR429W	94	0.35999	Saccharomyces cerevisiae	[ui:ylr429w] [pn:similarity to actin binding protein coronin] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5759	957936_c1_17	6539	20642	1515	505	YLR429W	1505	2.0(10)-154	Saccharomyces cerevisiae	[ui:ylr429w] [pn:similarity to actin binding protein coronin] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5739	24804528_c3_33	6540	20643	1182	394	YML104C	392	1.7(10)-36	Saccharomyces cerevisiae	[ui:ym104c] [pn:intermediate filament protein:structural protein mdm1] [gn:mdm1_ym8339] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b3x14621.y	21955093_f1_1	6541	20644	528	176	YML085C	647	1.6(10)-63	Saccharomyces cerevisiae	[ui:ym1085c] [pn:alpha-1 tubulin:tubulin alpha-1 chain] [gn:tub1] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5543	4772652_c3_19	6542	20645	1359	453	YMR033W	389	3.6(10)-36	Saccharomyces cerevisiae	[ui:ymr033w] [pn:actin-related protein] [gn:arp9] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4982	22298162_f1_4	6543	20646	1863	621	YMR092C	914	8.3(10)-92	Saccharomyces cerevisiae	[ui:ymr092c] [pn:actin cytoskeleton component:actin interacting protein 1] [gn:aipl_ym9582] [gtcf:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3926	5897562_f2_2	6544	20647	1413	471	YMR109W	1572	1.6(10)-161	Saccharomyces cerevisiae	[ui:ymr109w] [pn:myosin ii] [gn:myo5] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5038	15727137_c3_7	6545	20648	612	204	YMR109W	104	0.00018	Saccharomyces cerevisiae	[ui:ymr109w] [pn:myosin ii] [gn:myo5] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
blx19775.y	5319525_f3_2	6546	20649	474	158	YMR109W	303	1.1(10)-25	Saccharomyces cerevisiae	[ui:ymr109w] [pn:myosin ii] [gn:myo5] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1080	34408180_c3_5	6547	20650	423	141	YMR138W	200	3.7(10)-16	Saccharomyces cerevisiae	[ui:ymr138w] [pn:gtp-binding protein:gtp-binding protein cin4] [gn:cin4:gtp1:ugx1:ym9375] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3524	34236641_f2_1	6548	20651	1980	660	YNL271C	420	9.0(10)-50	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bnl1 protein:synthetic lethal 39] [gn:bnl1:she5:n0646] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4299	11760912_c1_3	6549	20652	1815	605	YNL271C	1201	3.1(10)-121	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bnl1 protein:synthetic lethal 39] [gn:bnl1:she5:n0646] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5680	10797577_c3_46	6550	20653	699	233	YNL271C	219	1.8(10)-16	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bnl1 protein:synthetic lethal 39] [gn:bnl1:she5:n0646] [gtcf:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5680	12890627_c3_45	6551	20654	3873	1291	YNL271C	687	4.4(10)-78	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bni1 protein:synthetic lethal 39] [gn:bni1:she5:n0646] [gcfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4986	36522702_c3_11	6552	20655	1002	334	YNL243W	439	2.0(10)-40	Saccharomyces cerevisiae	[ui:ynl243w] [pn:cytoskeleton assembly control protein:slaz protein:transmembrane protein mop2] [gn:slaz:end4:mop2:ufl1:n1102] [gcfc:12.16:12.6:12.8:12.9] [keggfc:14.2] [sgdfe:3.2.0:3.3.0:6.4.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4986	20509442_c2_9	6553	20656	2001	667	YNL243W	377	3.3(10)-58	Saccharomyces cerevisiae	[ui:ynl243w] [pn:cytoskeleton assembly control protein:slaz protein:transmembrane protein mop2] [gn:slaz:end4:mop2:ufl1:n1102] [gcfc:12.16:12.6:12.8:12.9] [keggfc:14.2] [sgdfe:3.2.0:3.3.0:6.4.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	23605000_c3_32	6554	20657	1746	582	YNL138W	1039	4.7(10)-105	Saccharomyces cerevisiae	[ui:ynl138w] [pn:adenylate cyclase-associated protein, 70kda:adenylate cyclase-associated protein:cap] [gn:sv2:cap1:n1210:n1838] [gcfc:12.16:12.8] [keggfc:14.2] [sgdfe:3.1.0:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5591	13828377_f3_8	6555	20658	1227	409	YNL084C	473	1.8(10)-52	Saccharomyces cerevisiae	[ui:ynl084c] [pn:required for endocytosis and cytoskeletal organization: end3 protein] [gn: end3:n2307] [gcfc: 12.16:12.6:12.8:12.9] [kegfc: 14.2] [sgdfe: 3.2.0:3.3.0:8.7.0:9.3.0] [db: gtc-saccharomyces cerevisiae]
CONTIG2630	7062807_f3_3	6556	20659	1137	379	YNL079C	181	1.3(10)-13	Saccharomyces cerevisiae	[ui:ynl079c] [pn: tropomyosin 1] [gn: ipml:n2332] [gcfc: 12.16:12.8:12.9] [kegfc: 14.2] [sgdfe: 3.1.0:3.2.0:3.3.0:9.3.0] [db: gtc-saccharomyces cerevisiae]
CONTIG3587	24017307_f2_2	6557	20660	987	329	YNL079C	92	0.029	Saccharomyces cerevisiae	[ui:ynl079c] [pn: tropomyosin 1] [gn: ipml:n2332] [gcfc: 12.16:12.8:12.9] [kegfc: 14.2] [sgdfe: 3.1.0:3.2.0:3.3.0:9.3.0] [db: gtc-saccharomyces cerevisiae]
CONTIG5652	14657183_f3_13	6558	20661	390	130	YNL079C	96	8.1(10)-5	Saccharomyces cerevisiae	[ui:ynl079c] [pn: tropomyosin 1] [gn: ipml:n2332] [gcfc: 12.16:12.8:12.9] [kegfc: 14.2] [sgdfe: 3.1.0:3.2.0:3.3.0:9.3.0] [db: gtc-saccharomyces cerevisiae]
CONTIG4290	33785677_c3_11	6559	20662	420	140	YOR122C	492	4.4(10)-47	Saccharomyces cerevisiae	[ui:yor122c] [pn: profilin] [gn: pfy1:pfy:prt1:o3275.yor3275c] [gcfc: 12.16:12.8] [kegfc: 14.2] [sgdfe: 3.2.0:9.3.0] [db: gtc-saccharomyces cerevisiae]
CONTIG1543	16579002_c3_2	6560	20663	984	328	YOR141C	494	1.7(10)-46	Saccharomyces cerevisiae	[ui:yor141c] [pn: actin-related protein] [gn: arp8] [gcfc: 12.16] [kegfc: 14.2] [sgdfe: 9.3.0] [db: gtc-saccharomyces cerevisiae]

b3x14418.y	10119075_c1_6	6561	20664	789	263	YOR141C	149	2.0(10)-9	Saccharomyces cerevisiae	[ui:yor141c] [pn:actin-related protein] [gn:arp8] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2891	798311_c3_6	6562	20665	573	191	YOR156C	104	0.005	Saccharomyces cerevisiae	[ui:yor156c] [pn:interacts with cdc12p in 2-hybrid assay] [gn:nf1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.8.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]
b9x13h02.x	31879280_f3_1	6563	20666	495	165	YOR156C	179	9.3(10)-13	Saccharomyces cerevisiae	[ui:yor156c] [pn:interacts with cdc12p in 2-hybrid assay] [gn:nf1] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.2.0:3.8.0:3.9.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG2589	10172691_f3_2	6564	20667	1563	521	YOR349W	147	3.7(10)-16	Saccharomyces cerevisiae	[ui:yor349w] [pn:chromosome segregation protein:cin1 protein] [gn:cin1:06350] [gctc:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5212	4725882_f3_10	6565	20668	594	198	YOR367W	170	5.7(10)-13	Saccharomyces cerevisiae	[ui:yor367w] [pn:similarity to mammalian smooth muscle protein sm22] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5571	24406687_f2_10	6566	20669	1212	404	YPL105C	105	0.01499	Saccharomyces cerevisiae	[ui:ypl105c] [pn:similarity to smy2p] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG4430	4351557_c1_6	6567	20670	810	270	YPR034W	290	2.7(10)-25	Saccharomyces cerevisiae	[ui:ypr034w] [pn:similarity to actins] [gn:arp7] [gctc:12.16] [keggfc:14.2] [sgdfe:9.3.0] [db:gic-saccharomyces cerevisiae]

b2x16596.x	471041_f3_1	6568	20671	651	217	YAL058W	327	2.2(10)-29	Saccharomyces cerevisiae	[ui:yal058w] [pn:similarity to calnexins:calnexin homolog precursor] [gn:cne1.fun481] [gcf:12.16] [kegfc:14.2] [sgdfc:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4324	10586087_f1_2	6569	20672	768	256	YBL102W	257	3.5(10)-22	Saccharomyces cerevisiae	[ui:ybl102w] [pn:suppressor of sed5 is mutants:sft2 protein] [gn:sft2.yb10812] [gcf:12.16] [kegfc:14.2] [sgdfc:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5516	2112580_f2_4	6570	20673	351	117	YBL102W	138	1.3(10)-9	Saccharomyces cerevisiae	[ui:ybl102w] [pn:suppressor of sed5 is mutants:sft2 protein] [gn:sft2.yb10812] [gcf:12.16] [kegfc:14.2] [sgdfc:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5516	16679015_f1_1	6571	20674	342	114	YBL102W	116	5.2(10)-7	Saccharomyces cerevisiae	[ui:ybl102w] [pn:suppressor of sed5 is mutants:sft2 protein] [gn:sft2.yb10812] [gcf:12.16] [kegfc:14.2] [sgdfc:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG2210	33759380_c2_5	6572	20675	510	170	YDR297W	531	3.2(10)-51	Saccharomyces cerevisiae	[ui:ydr297w] [pn:suppressor of rvs161 and rvs167 mutations:sur2 protein:2] [gn:sur2.syr2.d9740] [gcf:12.16:12.8] [kegfc:14.2] [sgdfc:3.2.0:9.4.0] [db:gic-saccharomyces cerevisiae]



CONTIG5308	432937_fl_3	6573	20676	765	255	YEL036C	908	3.6(10)-91	Saccharomyces cerevisiae	[ui:yei036c] [pn:protein of the endoplasmatic reticulum:aminonitrophenyl propanediol resistance protein] [gn:anp1:gem3:sygp-or728] [gicfc:12.16] [kegfc:14.2] [sgdfe:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4573	15631461_fl_5	6574	20677	306	102	YGR105W	192	2.7(10)-15	Saccharomyces cerevisiae	[ui:ygr105w] [pn:atpase assembly integral membrane protein, vacuolar:vacuolar atpase assembly integral membrane protein] [gn:yma2.1] [gicfc:12.16] [kegfc:14.2] [sgdfe:6.4.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4999	4332936_cl_8	6575	20678	579	193	YKL065C	176	1.3(10)-13	Saccharomyces cerevisiae	[ui:ykl065c] [pn:yeast endoplasmic reticulum 25 kda transmembrane protein:hyprothetical 23.4 kd protein in nup100-msn4 intergenic region] [gn:yel1:ykl33.1] [gicfc:12.16] [kegfc:14.2] [sgdfe:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5673	33765927_fl_4	6576	20679	723	241	YKL065C	136	5.2(10)-8	Saccharomyces cerevisiae	[ui:ykl065c] [pn:yeast endoplasmic reticulum 25 kda transmembrane protein:hyprothetical 23.4 kd protein in nup100-msn4 intergenic region] [gn:yel1:ykl33.1] [gicfc:12.16] [kegfc:14.2] [sgdfe:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4257	22460061_f2_1	6577	20680	972	324	YLR220W	674	2.2(10)-66	Saccharomyces cerevisiae	[ui:ylr220w] [pn:involved in calcium regulation:cccl protein] [gn:ccc1:l8083] [gicfc:12.16:12.6] [keggfc:14.2] [sgdfc:1.8.2:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3782	23439035_c1_3	6578	20681	1236	412	YDR080W	418	3.8(10)-38	Saccharomyces cerevisiae	[ui:ydr080w] [pn:required for the vacuolar assembly:hypothetical 113.4 kd protein in sed1-pdc2 intergenic region] [gn:yam2:d4446] [gicfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG5593	23484375_f3_11	6579	20682	663	221	YDR080W	404	1.2(10)-36	Saccharomyces cerevisiae	[ui:ydr080w] [pn:required for the vacuolar assembly:hypothetical 113.4 kd protein in sed1-pdc2 intergenic region] [gn:yam2:d4446] [gicfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG2592	14540931_f1_2	6580	20683	897	299	YGL212W	173	2.2(10)-11	Saccharomyces cerevisiae	[ui:ygl212w] [pn:vacuolar morphogenesis protein:protein] [gn:yam7] [gicfc:12.16] [keggfc:14.2] [sgdfc:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG5635	801000_f3_9	6581	20684	861	287	YGL212W	114	0.00021	Saccharomyces cerevisiae	[ui:ygl212w] [pn:vacuolar morphogenesis protein:protein] [gn:yam7] [gicfc:12.16] [keggfc:14.2] [sgdfc:9.10.0] [db:gic-saccharomyces cerevisiae]

CONTIG2568	4022782_c3_3	6582	20685	636	212	YHR026W	582	1.3(10)-56	Saccharomyces cerevisiae	[ui:YHR026W] [pn:h+-atpase 23 kd subunit, vacuolar:proteolipid protein] [gn:YMA16:PPA1] [gtcf:12.16:12.5:12.6] [kegfc:14.2] [sgdfc:7.2:7.8:0.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4735	16423305_c3_9	6583	20686	675	225	YKL119C	194	1.6(10)-15	Saccharomyces cerevisiae	[ui:YKL119C] [pn:h+-atpase assembly protein, vacuolar:vacuolar atpase assembly integral membrane protein YMA12:protein YPH2] [gn:YMA12:YPH2:CLS10:YKL520] [gtcf:12.16] [kegfc:14.2] [sgdfc:6.4:0.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1187	9853437_c3_3	6584	20687	714	238	YMR231W	222	1.3(10)-33	Saccharomyces cerevisiae	[ui:YMR231W] [pn:vacuolar biogenesis protein:vacuolar biogenesis protein END1:pep5 protein] [gn:END1:PEP5:YPS11:YMR959] [gtcf:12.16:12.6] [kegfc:14.2] [sgdfc:8.7:0.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1517	26444458_c3_1	6585	20688	828	276	YMR231W	233	7.2(10)-23	Saccharomyces cerevisiae	[ui:YMR231W] [pn:vacuolar biogenesis protein:vacuolar biogenesis protein END1:pep5 protein] [gn:END1:PEP5:YPS11:YMR959] [gtcf:12.16:12.6] [kegfc:14.2] [sgdfc:8.7:0.9:10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2609	915643_c2_3	6586	20689	534	178	YER060W	330	1.5(10)-29	Saccharomyces cerevisiae	[ui:yer060w-a] [pn:purine-cytosine permease:hypothetical 58.1 kd protein in pet17-cen1 intergenic region] [gn:fcy21:fcy] [gctc:12.16:12.3:12.6] [keggfc:14.2] [sgdfe:1.3.7:7.6:0.8:0.17:0.0] [db:gic-saccharomyces cerevisiae]
CONTIG2609	1213556_c3_4	6587	20690	702	234	YER060W-A	499	7.9(10)-48	Saccharomyces cerevisiae	[ui:yer060w-a] [pn:strong similarity to fcy2p] [gn:fcy22] [gctc:12.16:12.3:12.6] [keggfc:14.2] [sgdfe:1.3.7:7.6:0.8:0.17:0.0] [db:gic-saccharomyces cerevisiae]
CONTIG2609	34415702_c1_2	6588	20691	414	138	YER060W-A	194	1.3(10)-14	Saccharomyces cerevisiae	[ui:yer060w-a] [pn:strong similarity to fcy2p] [gn:fcy22] [gctc:12.16:12.3:12.6] [keggfc:14.2] [sgdfe:1.3.7:7.6:0.8:0.17:0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3872	4863500_f3_5	6589	20692	981	327	YOR100C	126	1.5(10)-5	Saccharomyces cerevisiae	[ui:yor100c] [pn:similarity to mitochondrial carrier protein ymc1] [gctc:12.16] [keggfc:14.2] [sgdfe:8.8:0] [db:gic-saccharomyces cerevisiae]
CONTIG4420	24037512_c2_7	6590	20693	876	292	YOR100C	747	4.0(10)-74	Saccharomyces cerevisiae	[ui:yor100c] [pn:similarity to mitochondrial carrier protein ymc1] [gctc:12.16] [keggfc:14.2] [sgdfe:8.8:0] [db:gic-saccharomyces cerevisiae]

CONTIG1621	24485906_f3_1	6591	20694	723	241	YBL037W	356	5.5(10)-34	Saccharomyces cerevisiae	[ui:ybl037w] [pn:alpha-adaptin, large subunit of the clathrin-associated protein:ap complex:alpha-adaptin homolog in ura7-pol12 intergenic region] [gn:ap13:ybl0412] [gicfc:12.16:12.6] [keggfc:14.2] [sgdfe:6.4.0:8.7.0] [db:gic-saccharo
CONTIG4408	12191910_c3_10	6592	20695	756	252	YBL037W	185	3.3(10)-13	Saccharomyces cerevisiae	[ui:ybl037w] [pn:alpha-adaptin, large subunit of the clathrin-associated protein:ap complex:alpha-adaptin homolog in ura7-pol12 intergenic region] [gn:ap13:ybl0412] [gicfc:12.16:12.6] [keggfc:14.2] [sgdfe:6.4.0:8.7.0] [db:gic-saccharo
CONTIG2516	4706642_c2_2	6593	20696	954	318	YDR162C	182	3.1(10)-14	Saccharomyces cerevisiae	[ui:ydr162c] [pn:nap1p-binding protein] [gn:nbp2] [gicfc:12.16] [keggfc:14.2] [sgdfe:6.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3342	23453211_f1_2	6594	20697	885	295	YDR265W	369	4.7(10)-34	Saccharomyces cerevisiae	[ui:ydr265w] [pn:peroxisomal assembly protein] [gn:pas4] [gicfc:12.16:12.6] [keggfc:14.2] [sgdfe:6.4.0:9.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5372	484675_c2_14	6595	20698	2115	705	YGR261C	490	1.6(10)-49	Saccharomyces cerevisiae	[ui:ygr261c] [pn:beta-adaptin, large subunit of the clathrin-associated protein:ap complex:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap16:yks5:g9331] [gic

CONTIG5670	13790932_f1_3	6596	20699	2028	676	YHR161C	447	2.2(10)-46	Saccharomyces cerevisiae	[ui:ylr161c] [pn:similarity to rat clathrin assembly protein ap180:hypothetical 71.7 kd protein in rec104-sol3 intergenic region] [gtcf:12.16] [keggfc:14.2] [sgdfc:6.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3178	29470261_c2_3	6597	20700	306	102	YJL024C	291	8.6(10)-26	Saccharomyces cerevisiae	[ui:yjl024c] [pn:clathrin-associated protein:ap complex, small subunit:probable adaptin complex small chain homolog] [gn:aps3:yks7:j1274] [gtcf:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3802	2788942_c1_5	6598	20701	189	63	YJL024C	128	1.6(10)-8	Saccharomyces cerevisiae	[ui:yjl024c] [pn:clathrin-associated protein:ap complex, small subunit:probable adaptin complex small chain homolog] [gn:aps3:yks7:j1274] [gtcf:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
blx14032.y	10032016_c3_2	6599	20702	792	264	YKL197C	273	1.3(10)-22	Saccharomyces cerevisiae	[ui:ykl197c] [pn:peroxisomal assembly protein:peroxisome biosynthesis protein] [gn:pas1] [gtcf:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5167	4454376_f2_4	6600	20703	282	94	YLR327C	190	4.4(10)-15	Saccharomyces cerevisiae	[ui:ylr327c] [pn:strong similarity to stf2p] [gtcf:12.16] [keggfc:14.2] [sgdfc:6.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2416	26751525_c3_6	6601	20704	1002	334	YNL329C	1003	3.1(10)-101	Saccharomyces cerevisiae	[ui:ynl329c] [pn:peroxisomal assembly protein:peroxisome biosynthesis protein pas8] [en:pas8:n0310] [gtcf:12.16:12.6] [kegfc:14.2] [sgdfc:6.4:0.9:8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3028	4422750_c2_4	6602	20705	1608	536	YPL195W	635	6.5(10)-62	Saccharomyces cerevisiae	[ui:yp1195w] [pn:alpha- or gamma-adaptin, large subunit of the clathrin-associated protein:ap complex] [en:yks4] [gtcf:12.16:12.6] [kegfc:14.2] [sgdfc:6.4:0.8:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG788	2460010_f2_2	6603	20706	441	147	YPL195W	409	3.1(10)-37	Saccharomyces cerevisiae	[ui:yp1195w] [pn:alpha- or gamma-adaptin, large subunit of the clathrin-associated protein:ap complex] [en:yks4] [gtcf:12.16:12.6] [kegfc:14.2] [sgdfc:6.4:0.8:7.0] [db:gtc-saccharomyces cerevisiae]
b2x16287.x	23469002_c3_2	6604	20707	732	244	YPR029C	128	4.2(10)-6	Saccharomyces cerevisiae	[ui:yp1029c] [pn:gamma-adaptin, large subunit of the clathrin-associated protein:ap complex] [en:ap14] [gtcf:12.16:12.6] [kegfc:14.2] [sgdfc:6.4:0.8:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1553	7313775_f1_1	6605	20708	513	171	YBR241C	425	5.5(10)-40	Saccharomyces cerevisiae	[ui:ybr241c] [pn:similarity to glucose transport proteins:probable metabolite transport protein ybr241c] [en:ybr1625] [gtcf:12.2:12.6] [kegfc:14.2] [sgdfc:1.5:3:7.3:0:17.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5225	5212782_c2_3	6606	20709	633	211	YBR241C	510	5.4(10)-49	Saccharomyces cerevisiae	[ui:ybr241c] [pn:similarity to glucose transport proteins:probable metabolite transport protein ybr241c] [gn:ybr1625] [gctc:12.2:12.6] [kegfc:14.2] [sgdfe:1.5.3:7.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5819	23540907_c2_50	6607	20710	1515	505	YBR241C	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ybr241c] [pn:similarity to glucose transport proteins:probable metabolite transport protein ybr241c] [gn:ybr1625] [gctc:12.2:12.6] [kegfc:14.2] [sgdfe:1.5.3:7.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5144	24392002_f3_3	6608	20711	1068	356	YDL199C	362	1.5(10)-32	Saccharomyces cerevisiae	[ui:ydl199c] [pn:similarity to sugar transporter proteins] [gctc:12.2:12.6] [kegfc:14.2] [sgdfe:1.5.3:7.3.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5348	6047337_c1_11	6609	20712	609	203	YDL138W	430	8.6(10)-40	Saccharomyces cerevisiae	[ui:ydl138w] [pn:suppressor of smf3 mutant] [gn:rg12] [gctc:12.2] [kegfc:14.2] [sgdfe:1.5.3:7.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5509	23652182_f1_2	6610	20713	1659	553	YDL138W	447	1.2(10)-41	Saccharomyces cerevisiae	[ui:ydl138w] [pn:suppressor of smf3 mutant] [gn:rg12] [gctc:12.2] [kegfc:14.2] [sgdfe:1.5.3:7.3.0] [db:gic-saccharomyces cerevisiae]



CONTIG2140	972311_c3_5	6611	20714	915	305	YFL040W	112	0.00129	Saccharomyces cerevisiae	[ui:yfl040w] [pn:similarity to yeast glucose transport proteins:probable metabolic transport protein yfl040w] [gtcf:12.2:12.6] [kegfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4937	29381925_c2_8	6612	20715	1215	405	YFR045W	231	4.5(10)-19	Saccharomyces cerevisiae	[ui:yfr045w] [pn:similarity to mitochondrial citrate transport proteins:putative mitochondrial carrier yfr045w] [gtcf:12.2] [kegfc:14.2] [sgdfc:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4958	35422157_c3_12	6613	20716	1353	451	YKL217W	673	2.8(10)-66	Saccharomyces cerevisiae	[ui:ykl217w] [pn:carboxylic acid transporter protein:carboxylic acid transporter protein homolog] [gn:jen1] [gtcf:12.2:12.6] [kegfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5497	7081302_c2_7	6614	20717	555	185	YKL217W	269	1.3(10)-22	Saccharomyces cerevisiae	[ui:ykl217w] [pn:carboxylic acid transporter protein:carboxylic acid transporter protein homolog] [gn:jen1] [gtcf:12.2:12.6] [kegfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG751	9942668_f3_1	6615	20718	645	215	YKL217W	316	1.1(10)-27	Saccharomyces cerevisiae	[ui:ykl217w] [pn:carboxylic acid transporter protein:carboxylic acid transporter protein homolog] [gn:jen1] [gtcf:12.2:12.6] [kegfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1708	16835882_c2_10	6616	20719	930	310	YOR271C	1072	1.5(10)-108	Saccharomyces cerevisiae	[lui:yor271c] [pn:strong similarity to ratius tricarboxylate carrier] [gtcf:12.2] [kegfc:14.2] [sgdfe:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1965	242312_f1_1	6617	20720	780	260	YOR271C	849	6.4(10)-85	Saccharomyces cerevisiae	[lui:yor271c] [pn:strong similarity to ratius tricarboxylate carrier] [gtcf:12.2] [kegfc:14.2] [sgdfe:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG854	14257050_c2_4	6618	20721	540	180	YBR041W	500	6.2(10)-48	Saccharomyces cerevisiae	[lui:ybr041w] [pn:similarity to m.musculus fatty acid transport protein:hypothetical 71.7 kd protein in figl-gip1 intergenic region] [gn:fat1:ybr041] [gtcf:12.2] [kegfc:14.2] [sgdfe:1.6.5.7.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG854	26567212_c2_3	6619	20722	282	94	YBR041W	211	2.6(10)-16	Saccharomyces cerevisiae	[lui:ybr041w] [pn:similarity to m.musculus fatty acid transport protein:hypothetical 71.7 kd protein in figl-gip1 intergenic region] [gn:fat1:ybr041] [gtcf:12.2] [kegfc:14.2] [sgdfe:1.6.5.7.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4552	26369586_c2_14	6620	20723	1185	395	YKL188C	430	2.7(10)-75	Saccharomyces cerevisiae	[lui:ykl188c] [pn:long-chain fatty acid transporter:peroxisomal long-chain fatty acid import protein 1] [gn:pat1:ykl174] [gtcf:12.2:12.6] [kegfc:14.2] [sgdfe:1.6.5.7.5.0:7.9.0:8.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4552	510285_c1_12	6621	20724	1107	369	YPL147W	208	9.5(10)-16	Saccharomyces cerevisiae	[ui:yp1147w] [pn:long-chain fatty acid transporter:peroxisomal long-chain fatty acid import protein 2] [gn:pat2:pxal:pal1:ssh2:ipi1w:p2607] [gicfc:12.2:12.6] [keggfc:14.2] [sgdfe:1.6.5:7.5:0.7:9.0:8.4:0:9.8.0] [db:gic-saccharomyces ce
CONTIG5470	5085003_c3_9	6622	20725	2316	772	YPL147W	895	4.4(10)-166	Saccharomyces cerevisiae	[ui:yp1147w] [pn:long-chain fatty acid transporter:peroxisomal long-chain fatty acid import protein 2] [gn:pat2:pxal:pal1:ssh2:ipi1w:p2607] [gicfc:12.2:12.6] [keggfc:14.2] [sgdfe:1.6.5:7.5:0.7:9.0:8.4:0:9.8.0] [db:gic-saccharomyces ce
CONTIG1202	2266557_c1_2	6623	20726	492	164	YDR142C	361	3.2(10)-33	Saccharomyces cerevisiae	[ui:ydr142c] [pn:peroxisomal import protein:peroxisome import protein pas7:peroxin 7] [gn:pas7:peb1:pex7:yd2943] [gicfc:12.2:12.6] [keggfc:14.2] [sgdfe:8.4:0:9.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3815	15038180_c3_7	6624	20727	282	94	YDR142C	277	2.6(10)-24	Saccharomyces cerevisiae	[ui:ydr142c] [pn:peroxisomal import protein:peroxisome import protein pas7:peroxin 7] [gn:pas7:peb1:pex7:yd2943] [gicfc:12.2:12.6] [keggfc:14.2] [sgdfe:8.4:0:9.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG2834	803312_c2_2	6625	20728	894	298	YGL186C	757	3.6(10)-75	Saccharomyces cerevisiae	[ui:yg1186c] [pn:similarity to hypothetical protein fcy21p and weak similarity to fcy2 protein: hypothetical 64.5 kd protein in cox4-gis1 intergenic region] [gn:g1370] [gtcf:12.3:12.6] [kegfc:14.2] [sgdfc:1.3.7:7.6.0:17.0.0] [db:gtc-
CONTIG5642	12148577_f2_2	6626	20729	1587	529	YGL186C	1007	3.0(10)-118	Saccharomyces cerevisiae	[ui:yg1186c] [pn:similarity to hypothetical protein fcy21p and weak similarity to fcy2 protein: hypothetical 64.5 kd protein in cox4-gis1 intergenic region] [gn:g1370] [gtcf:12.3:12.6] [kegfc:14.2] [sgdfc:1.3.7:7.6.0:17.0.0] [db:gtc-
b9x10393.y	4335156_c1_1	6627	20730	534	178	YGL186C	300	5.0(10)-26	Saccharomyces cerevisiae	[ui:yg1186c] [pn:similarity to hypothetical protein fcy21p and weak similarity to fcy2 protein: hypothetical 64.5 kd protein in cox4-gis1 intergenic region] [gn:g1370] [gtcf:12.3:12.6] [kegfc:14.2] [sgdfc:1.3.7:7.6.0:17.0.0] [db:gtc-
CONTIG4416	23553827_f1_1	6628	20731	906	302	YGR096W	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:Ygr096w] [pn:similarity to bovine graves disease carrier protein: putative mitochondrial carrier Ygr096w] [gtcf:12.3] [kegfc:14.2] [sgdfc:1.3.7:7.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5156	21994017_c3_14	6629	20732	339	113	YHR002W	159	3.6(10)-11	Saccharomyces cerevisiae	[ui:yhr002w] [pn:similarity to bovine mitochondrial carrier protein/grave's disease carrier protein:putative mitochondrial carrier yhr002w] [gtcf:12.3] [kegfc:14.2] [sgdfe:1.3:7.7:6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4092	4103578_f1_1	6630	20733	810	270	YPR011C	653	3.7(10)-64	Saccharomyces cerevisiae	[ui:ypr011c] [pn:similarity to adp/atp carrier proteins and graves disease carrier protein] [gtcf:12.3] [kegfc:14.2] [sgdfe:1.3:7.7:6.0] [db:gic-saccharomyces cerevisiae]
CONTIG3292	24395161_f2_2	6631	20734	579	193	YPR011C	163	1.0(10)-11	Saccharomyces cerevisiae	[ui:ypr011c] [pn:similarity to adp/atp carrier proteins and graves disease carrier protein] [gtcf:12.3] [kegfc:14.2] [sgdfe:1.3:7.7:6.0] [db:gic-saccharomyces cerevisiae]
CONTIG1318	32462785_f2_3	6632	20735	267	89	YBR235W	208	1.3(10)-15	Saccharomyces cerevisiae	[ui:ybr235w] [pn:similarity to bumetanide-sensitive na-k-cl cotransport protein:hyprothetical 124.0 kd protein in pcs60-abd1 intergenic region] [gn:ybr1601] [gtcf:12.4:12.5:12.6] [kegfc:14.2] [sgdfe:1.8:2:7.2:2.3:17.0:0] [db:gic-

CONTIG2248	34094015_f2_1	6633	20736	1458	486	YBR235W	268	3,6(10)-20	Saccharomyces cerevisiae	[ui:ybr235w] [pn:similarity to bumetanide-sensitive na-k-cl cotransport protein:hypothetical 124.0 kd protein in pcs60-abd1 intergenic region] [gn:ybr1601] [gtcf:12.4:12.5:12.6] [kegfc:14.2] [sgdfc:1.8.2:7.2:2.3:17.0.0] [db:gtc-
CONTIG3606	14644442_c1_5	6634	20737	1434	478	YBR235W	1191	3,7(10)-121	Saccharomyces cerevisiae	[ui:ybr235w] [pn:similarity to bumetanide-sensitive na-k-cl cotransport protein:hypothetical 124.0 kd protein in pcs60-abd1 intergenic region] [gn:ybr1601] [gtcf:12.4:12.5:12.6] [kegfc:14.2] [sgdfc:1.8.2:7.2:2.3:17.0.0] [db:gtc-
CONTIG5398	20351377_f1_4	6635	20738	1530	510	YBR296C	988	9,3(10)-141	Saccharomyces cerevisiae	[ui:ybr296c] [pn:strong similarity to phosphate-repressible phosphate permease:putative phosphate-repressible phosphate permease ybr29c] [gn:ybr2113] [gtcf:12.4:12.6:13.10] [kegfc:14.2] [sgdfc:1.4.3:1.8.2:7.2:3:17.0.0] [db:gtc-sacch
CONTIG1600	26376660_f1_2	6636	20739	792	264	YCR037C	368	7,5(10)-33	Saccharomyces cerevisiae	[ui:ycr037c] [pn:member of the phosphate permease family:inorganic phosphate transporter pho87] [gn:pho87.ycr37c.ycr524] [gtcf:12.4:13.10] [kegfc:14.2] [sgdfc:1.4.3:1.8.2:7.2:3:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2512	783532_c1_2	6637	20740	504	168	YCR037C	519	3.8(10)-49	Saccharomyces cerevisiae	[ui:ycr037c] [pn:member of the phosphate permease family:inorganic phosphate transporter pho87] [gn:pho87:ycr37c:ycr524] [gcfc:12.4:13.10] [kegfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x14152.x	210967_c3_3	6638	20741	969	323	YCR037C	256	7.7(10)-21	Saccharomyces cerevisiae	[ui:ycr037c] [pn:member of the phosphate permease family:inorganic phosphate transporter pho87] [gn:pho87:ycr37c:ycr524] [gcfc:12.4:13.10] [kegfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2431	20486557_c2_6	6639	20742	246	82	YJL198W	144	6.7(10)-9	Saccharomyces cerevisiae	[ui:yjl198w] [pn:strong similarity to pho87p:hypothetical 97.7 kd membrane protein in prp21-ubp12 intergenic region] [gn:j0336] [gcfc:12.4:12.6:13.10] [kegfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2844	14178762_c2_5	6640	20743	960	320	YJL198W	105	0.01299	Saccharomyces cerevisiae	[ui:yjl198w] [pn:strong similarity to pho87p:hypothetical 97.7 kd membrane protein in prp21-ubp12 intergenic region] [gn:j0336] [gcfc:12.4:12.6:13.10] [kegfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1635	24804812_f1_1	6641	20744	729	243	YJL117W	162	1.2(10)-10	Saccharomyces cerevisiae	[ui:yj117w] [pn:inorganic phosphate transporter:inorganic phosphate transporter pho86] [gn:pho86;j0744] [gtcf:12.4:13.10] [keggfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG481	10579187_c3_3	6642	20745	219	73	YJL117W	97	0.00017	Saccharomyces cerevisiae	[ui:yj117w] [pn:inorganic phosphate transporter:inorganic phosphate transporter pho86] [gn:pho86;j0744] [gtcf:12.4:13.10] [keggfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG5446	14881535_f1_2	6643	20746	2487	829	YLR092W	1744	9.3(10)-180	Saccharomyces cerevisiae	[ui:yhr092w] [pn:strong similarity to sul1p] [gn:se12] [gtcf:12.4:12.6] [keggfc:14.2] [sgdfe:1.2.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3415	788317_f1_1	6644	20747	765	255	YNR013C	118	0.00032	Saccharomyces cerevisiae	[ui:ynr013c] [pn:similarity to membrane protein pho87p and hypothetical protein yj1198w:hypothetical 99.5 kd protein in urk1-smm1 intergenic region] [gn:n2052] [gtcf:12.4:12.6:13.10] [keggfc:14.2] [sgdfe:1.4.3:1.8.2:7.2.3:17.0.0] [db



CONTIG3530	11876286_c2_6	6645	20748	264	88	YNR013C	165	3.8(10)-11	Saccharomyces cerevisiae	[ui:ynr013c] [pn:similarity to membrane protein pho87p and hypothetical protein yjl198w:hypothetical 99.5 kd protein in urk1-smn1 intergenic region] [gn:n2052] [gtcf:12.4:12.6:13.10] [kegfc:14.2] [sgdfe:1.4.3:1.8.2.7.2.3:17.0.0] [db
CONTIG2761	4039134_c1_2	6646	20749	1266	422	YNR013C	1153	3.8(10)-117	Saccharomyces cerevisiae	[ui:ynr013c] [pn:similarity to membrane protein pho87p and hypothetical protein yjl198w:hypothetical 99.5 kd protein in urk1-smn1 intergenic region] [gn:n2052] [gtcf:12.4:12.6:13.10] [kegfc:14.2] [sgdfe:1.4.3:1.8.2.7.2.3:17.0.0] [db
CONTIG3466	4475255_c3_4	6647	20750	420	140	YPR138C	343	2.7(10)-31	Saccharomyces cerevisiae	[ui:yp138c] [pn:strong similarity to ammonium transport proteins:ammonium transporter mep3] [gn:mep3:p9659] [gtcf:12.5] [kegfc:14.2] [sgdfe:1.2.3:7.2.2:17.0.0] [db:gtc-saccharomyces cerevisiae]
b9x10b25.x	31407754_c2_2	6648	20751	528	176	YPR138C	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:yp138c] [pn:strong similarity to ammonium transport proteins:ammonium transporter mep3] [gn:mep3:p9659] [gtcf:12.5] [kegfc:14.2] [sgdfe:1.2.3:7.2.2:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG238	4375052_c3_1	6649	20752	678	226	YAL026C	792	5.9(10)-78	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.2.2:7.8.0] [db:gtc-sac
CONTIG2297	26367325_c1_3	6650	20753	975	325	YAL026C	1093	9.0(10)-111	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.2.2:7.8.0] [db:gtc-sac
CONTIG3268	5906250_c2_7	6651	20754	1353	451	YAL026C	761	1.3(10)-74	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.2.2:7.8.0] [db:gtc-sac
CONTIG5035	483516_c3_15	6652	20755	390	130	YAL026C	319	2.6(10)-27	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.2.2:7.8.0] [db:gtc-sac

CONTIG5397	24413193_c1_18	6653	20756	684	228	YDR456W	611	1.1(10)-59	Saccharomyces cerevisiae	[ui:Ydr456w] [pn:similarity to mammalian na <sup>+</sup> -h <sup>+</sup> antiporters] [gtcf:12.5:12.6] [kegfc:14.2] [sgdfe:1.8.2:7.2.2:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1608	23879781_c3_9	6654	20757	948	316	YLR138W	433	1.1(10)-45	Saccharomyces cerevisiae	[ui:Ylr138w] [pn:putative na <sup>+</sup> -h <sup>+</sup> antiporter] [gn:nha1] [gtcf:12.5:12.6] [kegfc:14.2] [sgdfe:1.8.2:7.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5606	7115936_f3_23	6655	20758	1239	413	YLR138W	1185	1.6(10)-120	Saccharomyces cerevisiae	[ui:Ylr138w] [pn:putative na <sup>+</sup> -h <sup>+</sup> antiporter] [gn:nha1] [gtcf:12.5:12.6] [kegfc:14.2] [sgdfe:1.8.2:7.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5606	35180166_f2_15	6656	20759	1434	478	YLR138W	465	5.4(10)-58	Saccharomyces cerevisiae	[ui:Ylr138w] [pn:putative na <sup>+</sup> -h <sup>+</sup> antiporter] [gn:nha1] [gtcf:12.5:12.6] [kegfc:14.2] [sgdfe:1.8.2:7.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4942	29330192_c3_24	6657	20760	1653	551	YDR091C	2313	4.7(10)-240	Saccharomyces cerevisiae	[ui:Ydr091c] [pn:strong similarity to human mrase 1 inhibitor and m.jannaschii abc transporter protein] [gtcf:12.6:10.2] [kegfc:14.2] [sgdfe:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1100	19562952_c1_1	6658	20761	627	209	YDR406W	414	2.2(10)-37	Saccharomyces cerevisiae	[ui:Ydr406w] [pn:atp-binding cassette transporter family member] [gn:pdrl5] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5296	26797286_c2_12	6659	20762	1833	611	YDR406W	1504	2.5(10)-154	Saccharomyces cerevisiae	[ui:ydr406w] [pn:atp-binding cassette transporter family member] [gn:ptr15] [gctc:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:glc-saccharomyces cerevisiae]
CONTIG5296	865925_c3_14	6660	20763	804	268	YDR406W	486	4.9(10)-45	Saccharomyces cerevisiae	[ui:ydr406w] [pn:atp-binding cassette transporter family member] [gn:ptr15] [gctc:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:glc-saccharomyces cerevisiae]
CONTIG5761	5101436_f3_12	6661	20764	1842	614	YER036C	2436	4.2(10)-253	Saccharomyces cerevisiae	[ui:yer036c] [pn:similarity to members of the abc transporter family:probable atp-dependent transporter yer036c] [gctc:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:glc-saccharomyces cerevisiae]
CONTIG3011	25425802_c2_8	6662	20765	843	281	YFL028C	657	1.3(10)-64	Saccharomyces cerevisiae	[ui:yfl028c] [pn:atp-binding cassette transporter family member:probable atp-dependent transporter yfl028c] [gn:caf16] [gctc:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:glc-saccharomyces cerevisiae]
CONTIG4658	15907831_c3_7	6663	20766	825	275	YFL028C	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:yfl028c] [pn:atp-binding cassette transporter family member:probable atp-dependent transporter yfl028c] [gn:caf16] [gctc:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:glc-saccharomyces cerevisiae]
CONTIG4530	14570388_f3_4	6664	20767	276	92	YLL048C	263	3.1(10)-21	Saccharomyces cerevisiae	[ui:yll048c] [pn:similarity to rat organic anion transporter] [gctc:12.4:12.6] [kegfc:14.2] [sgdfe:7.9.0] [db:glc-saccharomyces cerevisiae]

CONTIG2029	20320275_c1_1	6665	20768	336	112	YLR188W	277	2.5(10)-23	Saccharomyces cerevisiae	[ui:y/r188w] [pn:atp-binding cassette transporter family member:atp-dependent permease mdl1] [gn:mdl1:19470] [gctc:12.6:1.1] [keggfc:14.2] [sgdfe:7.9.0] [db:gic-saccharomyces cerevisiae]
b3x19039.x	20019533_f2_1	6666	20769	501	167	YLR188W	412	5.2(10)-38	Saccharomyces cerevisiae	[ui:y/r188w] [pn:atp-binding cassette transporter family member:atp-dependent permease mdl1] [gn:mdl1:19470] [gctc:12.6:1.1] [keggfc:14.2] [sgdfe:7.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4368	34023325_c3_7	6667	20770	900	300	YOL075C	443	1.0(10)-40	Saccharomyces cerevisiae	[ui:yol075c] [pn:similarity to a.gambiae atp-binding-cassette protein] [gctc:12.6] [keggfc:14.2] [sgdfe:7.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4643	23859467_f2_2	6668	20771	861	287	YOL075C	434	9.3(10)-40	Saccharomyces cerevisiae	[ui:yol075c] [pn:similarity to a.gambiae atp-binding-cassette protein] [gctc:12.6] [keggfc:14.2] [sgdfe:7.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4643	21912952_f3_4	6669	20772	1557	519	YOL075C	918	3.1(10)-92	Saccharomyces cerevisiae	[ui:yol075c] [pn:similarity to a.gambiae atp-binding-cassette protein] [gctc:12.6] [keggfc:14.2] [sgdfe:7.9.0] [db:gic-saccharomyces cerevisiae]

CONTIG4029	819077_c2_8	6670	20773	2232	744	YPL270W	1053	1.6(10)-106	Saccharomyces cerevisiae	[ui:yp1270w] [pn:atp-binding cassette:abc transporter family member:atp-dependent permease mdl2] [gn:mdl2:ssh1] [gtcf:12.6:1.1] [kegfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5597	2142151_c3_21	6671	20774	1278	426	YBR290W	450	1.2(10)-42	Saccharomyces cerevisiae	[ui:ybr290w] [pn:metal homeostasis protein:metal homeostatis protein bsd2] [gn:bsd2:ybr2037] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1:7.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5220	25394527_c1_8	6672	20775	423	141	YDR270W	316	3.3(10)-27	Saccharomyces cerevisiae	[ui:ydr270w] [pn:probable copper-transporting atpase] [gn:ccc2] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1:7.2.1:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5220	11134712_c1_7	6673	20776	2880	960	YDR270W	558	7.0(10)-91	Saccharomyces cerevisiae	[ui:ydr270w] [pn:probable copper-transporting atpase] [gn:ccc2] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1:7.2.1:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5221	4723903_c1_16	6674	20777	1911	637	YDR270W	173	5.4(10)-16	Saccharomyces cerevisiae	[ui:ydr270w] [pn:probable copper-transporting atpase] [gn:ccc2] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1:7.2.1:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1580	34236641_f3_3	6675	20778	369	123	YLR130C	90	0.0016	Saccharomyces cerevisiae	[ui:yrl130c] [pn:low affinity zinc transporter] [gn:zrt2] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1:7.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5819	5895067_f2_5	6676	20779	387	129	YLR130C	442	8.6(10)-42	Saccharomyces cerevisiae	[ui:ylr130c] [pn:low affinity zinc transporter] [gn:zrt2] [gcfc:12.6] [kegfc:14.2] [sgdfe:1.8:1.7.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG2369	4490632_c1_4	6677	20780	1035	345	YAL067C	406	7.0(10)-38	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxide ethionine resistance:hypothetical 68.8 kd protein in gdh3 5' region] [gn:seo1] [gcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.7.0:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4389	3016876_c1_4	6678	20781	246	82	YAL067C	168	1.0(10)-11	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxide ethionine resistance:hypothetical 68.8 kd protein in gdh3 5' region] [gn:seo1] [gcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.7.0:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4389	555342_c3_6	6679	20782	1293	431	YAL067C	792	7.0(10)-79	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxide ethionine resistance:hypothetical 68.8 kd protein in gdh3 5' region] [gn:seo1] [gcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.7.0:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5195	22558275_c1_8	6680	20783	861	287	YAL067C	777	2.7(10)-77	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5'region] [gn:seo1] [gdcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.7.0:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5195	9798555_c3_9	6681	20784	1092	364	YAL067C	682	3.2(10)-67	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5'region] [gn:seo1] [gdcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.7.0:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5471	26462875_f3_8	6682	20785	663	221	YAL067C	187	9.3(10)-14	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5'region] [gn:seo1] [gdcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.7.0:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5813	9875126_c2_47	6683	20786	396	132	YMR123W	179	6.4(10)-14	Saccharomyces cerevisiae	[ui:ymr123w] [pn:resistance against pitchia farinosa killer toxin:smk toxin when expressed by a multi copy plasmid] [gn:pkr1] [gdcfc:12.6:13.3] [kegfc:14.2] [sgdfe:7.10.0:17.0.0] [db:gic-saccharomyces cerevisiae]



CONTIG4533	16220688_c2_5	6684	20787	2466	822	YDR093W	2400	2.7(10)-249	Saccharomyces cerevisiae	[ui:ydr093w] [pn:similarity to p.falciptarum atpase 2;probable calcium-transporting atpase 4] [gn:drs2.yd8557] [gtcf:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4834	26445187_f3_4	6685	20788	2445	815	YDR093W	1527	9.1(10)-157	Saccharomyces cerevisiae	[ui:ydr093w] [pn:similarity to p.falciptarum atpase 2;probable calcium-transporting atpase 4] [gn:drs2.yd8557] [gtcf:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG326	33695388_c3_3	6686	20789	555	185	YER166W	606	8.0(10)-58	Saccharomyces cerevisiae	[ui:yer166w] [pn:similarity to atpase p.falciptarum atpase 2;probable calcium-transporting atpase 5] [gn:sygp-or7] [gtcf:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4501	4031306_c1_9	6687	20790	390	130	YER166W	240	8.1(10)-19	Saccharomyces cerevisiae	[ui:yer166w] [pn:similarity to atpase p.falciptarum atpase 2;probable calcium-transporting atpase 5] [gn:sygp-or7] [gtcf:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG608	4814625_c3_1	6688	20791	501	167	YER166W	515	4.2(10)-48	Saccharomyces cerevisiae	[ui:yer166w] [pn:similarity to atpase p.falciptarum atpase 2;probable calcium-transporting atpase 5] [gn:sygp-or7] [gtcf:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3066	12790912_c3_10	6689	20792	2457	819	YMR162C	1665	2.2(10)-171	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to apases] [gcfc:12.6] [keggfc:14.2] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5758	26812517_c2_21	6690	20793	990	330	YMR162C	386	2.5(10)-34	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to apases] [gcfc:12.6] [keggfc:14.2] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
blx15548.x	23631392_c2_3	6691	20794	579	193	YMR162C	463	1.6(10)-42	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to apases] [gcfc:12.6] [keggfc:14.2] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1020	5085349_c1_3	6692	20795	993	331	YMR162C	623	1.3(10)-59	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to apases] [gcfc:12.6] [keggfc:14.2] [sgdfe:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1766	7313802_fl_1	6693	20796	801	267	YGR260W	229	2.2(10)-18	Saccharomyces cerevisiae	[ui:ygr260w] [pn:similarity to allantoate transport protein:hypothetical 60.1 kd protein in rad2-apl6 intergenic region] [gcfc:12.6] [keggfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4034	175056_c1_4	6694	20797	1446	482	YGR260W	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:ygr260w] [pn:similarity to allantoate transport protein:hypothetical 60.1 kd protein in rad2-apl6 intergenic region] [gcfc:12.6] [keggfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3312	7057_fl_1	6695	20798	1533	511	YIL166C	1028	6.9(10)-104	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hyprothetical 61.9 kd protein in suc2 5' region] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5018	25446900_c3_19	6696	20799	1242	414	YIL166C	859	5.5(10)-86	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hyprothetical 61.9 kd protein in suc2 5' region] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5018	12929035_c3_18	6697	20800	324	108	YIL166C	109	2.0(10)-5	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hyprothetical 61.9 kd protein in suc2 5' region] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG5818	6035255_fl_2	6698	20801	1794	598	YIL166C	1074	9.1(10)-109	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hyprothetical 61.9 kd protein in suc2 5' region] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3436	34158510_fl_3	6699	20802	1254	418	YLR004C	467	1.8(10)-44	Saccharomyces cerevisiae	[ui:yilr004c] [pn:similarity to allantoate transport protein] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5192	1304627_c3_17	6700	20803	1563	521	YLR004C	1244	8.9(10)-127	Saccharomyces cerevisiae	[ui:yhr004c] [pn:similarity to allantoinate transport protein] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4360	9954506_c1_3	6701	20804	681	227	YBL089W	230	1.0(10)-29	Saccharomyces cerevisiae	[ui:ybl089w] [pn:weak similarity to a thaliana aminoacid permease aap3: hypothetical 57.1 kd protein in map2-tell intergenic region] [gn:ybl0703] [gtcf:12.6] [kegfc:14.2] [sgdfe:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5736	1053127_f1_7	6702	20805	513	171	YBL011W	349	5.2(10)-31	Saccharomyces cerevisiae	[ui:ybl011w] [pn:suppresses a choline-transport mutant: hypothetical 85.7 kd protein in rno6-hirt intergenic region] [gn:set1:ybl0315:ybl0309] [gtcf:12.6:12.13] [kegfc:14.2] [sgdfe:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5736	24268805_f2_13	6703	20806	1794	598	YBL011W	1097	3.3(10)-111	Saccharomyces cerevisiae	[ui:ybl011w] [pn:suppresses a choline-transport mutant: hypothetical 85.7 kd protein in rno6-hirt intergenic region] [gn:set1:ybl0315:ybl0309] [gtcf:12.6:12.13] [kegfc:14.2] [sgdfe:7.11.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5819	35555166_c3_52	6704	20807	672	224	YBL011W	472	2.0(10)-44	Saccharomyces cerevisiae	[ui:ybl011w] [pn:suppresses a choline-transport mutant;hypothetical 85.7 kd protein in rrm6-hrt1 intergenic region] [gn:scell.yb10315.yb10309] [gtcf:12.6:12.13] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4250	3912830_c2_5	6705	20808	507	169	YDL206W	187	1.3(10)-13	Saccharomyces cerevisiae	[ui:ydl206w] [pn:weak similarity to transporter proteins] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4250	31796927_c3_6	6706	20809	1527	509	YDL206W	158	3.3(10)-8	Saccharomyces cerevisiae	[ui:ydl206w] [pn:weak similarity to transporter proteins] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG583	43867055_c3_2	6707	20810	624	208	YEL064C	456	2.7(10)-43	Saccharomyces cerevisiae	[ui:yel064c] [pn:similarity to yb1089w;hypothetical 53.3 kd protein in hx18-can1 intergenic region] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG12	24414062_c3_4	6708	20811	399	133	YER119C	250	6.2(10)-21	Saccharomyces cerevisiae	[ui:yer119c] [pn:weak similarity to e.herbicola tyrosine permease;hypothetical 48.8 kd protein in ssu81-scs2 intergenic region] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3058	24414062_f1_1	6709	20812	798	266	YER119C	413	1.0(10)-38	Saccharomyces cerevisiae	[ui:yer119c] [pn:weak similarity to e.therbicola tyrosine permease:hypothetical 48.8 kd protein in ssu81-ssc2 intergenic region] [gtcf:12.6] [keggfc:14.2] [sgdfe:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1878	9869051_c2_2	6710	20813	1200	400	YIL088C	684	1.3(10)-77	Saccharomyces cerevisiae	[ui:yi1088c] [pn:weak similarity to a.thaliana aminoacid permease aap4:hypothetical 53.7 kd protein in sgat-sds3 intergenic region] [gtcf:12.1:11.1] [keggfc:14.2] [sgdfe:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3768	816902_c3_4	6711	20814	720	240	YIL006W	432	9.9(10)-41	Saccharomyces cerevisiae	[ui:yi1006w] [pn:similarity to fix1p:putative mitochondrial carrier yil006w] [gtcf:12.6] [keggfc:14.2] [sgdfe:1.7.4:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3513	4970052_c3_10	6712	20815	1452	484	YJR001W	350	6.2(10)-56	Saccharomyces cerevisiae	[ui:yi001w] [pn:weak similarity to a.thaliana aminoacid permease aap4:hypothetical 65.3 kd protein in pre3-sag1 intergenic region] [gn:j1409:yi83] [gtcf:12.6] [keggfc:14.2] [sgdfe:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5231	5112760_f3_5	6713	20816	1536	512	YJR001W	865	1.3(10)-86	Saccharomyces cerevisiae	[ui:yi001w] [pn:weak similarity to a.thaliana aminoacid permease aap4:hypothetical 65.3 kd protein in pre3-sag1 intergenic region] [gn:j1409:yi83] [gtcf:12.6] [keggfc:14.2] [sgdfe:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1449	24422183_f3_2	6714	20817	471	157	YJR124C	259	6.0(10)-22	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hyprothetical 49.7 kd protein in pps5-zms1 intergenic region] [gn:j2046] [gtcf:12.6] [kegfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1449	29687515_f1_1	6715	20818	294	98	YJR124C	212	9.8(10)-17	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hyprothetical 49.7 kd protein in pps5-zms1 intergenic region] [gn:j2046] [gtcf:12.6] [kegfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3638	433325_g2_4	6716	20819	576	192	YJR124C	401	1.8(10)-37	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hyprothetical 49.7 kd protein in pps5-zms1 intergenic region] [gn:j2046] [gtcf:12.6] [kegfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5664	18887_f1_3	6717	20820	1443	481	YJR124C	573	1.1(10)-55	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hyprothetical 49.7 kd protein in pps5-zms1 intergenic region] [gn:j2046] [gtcf:12.6] [kegfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5288	4319661_f3_10	6718	20821	1332	444	YKL221W	793	5.5(10)-79	Saccharomyces cerevisiae	[ui:y:k1221w] [pn:weak similarity to human x-linked pest-containing transporter:hypothetical 52.3 kd protein in fre2 5"region] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG167	11776042_f1_1	6719	20822	864	288	YKL146W	245	3.2(10)-27	Saccharomyces cerevisiae	[ui:y:k1146w] [pn:strong similarity to s.pombe hypothetical protein c3h1.09c:hypothetical 75.5 kd protein in sdh1-cim5/yta3 intergenic region] [gn:y:k1600] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3818	32535156_c1_1	6720	20823	432	144	YKL146W	242	1.5(10)-19	Saccharomyces cerevisiae	[ui:y:k1146w] [pn:strong similarity to s.pombe hypothetical protein c3h1.09c:hypothetical 75.5 kd protein in sdh1-cim5/yta3 intergenic region] [gn:y:k1600] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5819	4375257_c3_53	6721	20824	1248	416	YKR067W	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:y:k067w] [pn:strong similarity to sc1p:hypothetical 83.6 kd protein in ccp1-sis2 intergenic region] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]



CONTIG4080	19539067_c3_6	6722	20825	1344	448	YNL125C	561	2.1(10)-54	Saccharomyces cerevisiae	[ui:ynl125c] [pn:similarity to yki1221w and human x-linked pest-containing transporter:hypothetical 73.8 kd protein in spe98-tom70 intergenic region] [gn:n1882:n1223:esbp6] [gtcf:12.6] [keggf:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-sacch]
CONTIG4189	1455090_f3_2	6723	20826	498	166	YNL125C	173	8.9(10)-16	Saccharomyces cerevisiae	[ui:ynl125c] [pn:similarity to yki1221w and human x-linked pest-containing transporter:hypothetical 73.8 kd protein in spe98-tom70 intergenic region] [gn:n1882:n1223:esbp6] [gtcf:12.6] [keggf:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-sacch]
CONTIG1652	20443932_f1_2	6724	20827	690	230	YNL003C	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ynl003c] [pn:similarity to mitochondrial rat tricarboxylate transport protein precursor:putative mitochondrial carrier protein pct8] [gn:pct8:n2012] [gtcf:12.6:1.2:12.16] [keggf:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1160	26582562_f2_2	6725	20828	423	141	YOL119C	216	4.7(10)-17	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcf:12.6] [keggf:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG19	7051302_c3_1	6726	20829	315	105	YOL119C	124	4.2(10)-7	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcf:12.6] [keggf:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4765	7051302_c1_7	6727	20830	984	328	YOL119C	510	5.4(10)-49	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG675	5312800_c1_2	6728	20831	1035	345	YOL119C	322	8.5(10)-29	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3557	20500024_c1_4	6729	20832	1146	382	YOL119C	716	8.0(10)-71	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4874	4117278_c3_6	6730	20833	1848	616	YOR291W	1395	8.9(10)-143	Saccharomyces cerevisiae	[ui:yor291w] [pn:similarity to cation translocating atpases] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	33650312_f2_18	6731	20834	1443	481	YOR291W	476	9.6(10)-59	Saccharomyces cerevisiae	[ui:yor291w] [pn:similarity to cation translocating atpases] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	24398450_f3_38	6732	20835	240	80	YOR291W	224	3.7(10)-17	Saccharomyces cerevisiae	[ui:yor291w] [pn:similarity to cation translocating atpases] [gtcf:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4492	22087875_c2_8	6733	20836	1437	479	YHL017W	104	0.019	Saccharomyces cerevisiae	[ui:yh017w] [pn:strong similarity to ptm1p;hypothetical 61.2 kd protein in apm2-dur3 intergenic region precursor] [gtcfc:12.6:14.3] [keggfc:14.2] [sgdfc:17.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4655	24431555_c3_2	6734	20837	1860	620	YHL017W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:yh017w] [pn:strong similarity to ptm1p;hypothetical 61.2 kd protein in apm2-dur3 intergenic region precursor] [gtcfc:12.6:14.3] [keggfc:14.2] [sgdfc:17.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG688	24431555_c2_2	6735	20838	447	149	YHL017W	123	6.0(10)-7	Saccharomyces cerevisiae	[ui:yh017w] [pn:strong similarity to ptm1p;hypothetical 61.2 kd protein in apm2-dur3 intergenic region precursor] [gtcfc:12.6:14.3] [keggfc:14.2] [sgdfc:17.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5638	23838432_c1_15	6736	20839	1767	589	YCL037C	96	0.05899	Saccharomyces cerevisiae	[ui:ycl037c] [pn:suppressor of rho3;hypothetical 51.8 kd protein in glk1-ste50 intergenic region] [gn:spo9ycl37c] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2117	14100916_f1_1	6737	20840	1107	369	YDR515W	114	0.00056	Saccharomyces cerevisiae	[ui:ydr515w] [pn:copper homeostasis protein] [gn:sif1] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4560	24095311_f2_1	6738	20841	336	112	YFL041W	217	5.9(10)-17	Saccharomyces cerevisiae	[ui:yf1041w] [pn:strong similarity to cell surface ferroxidase precursor fet3p;hypothetical 70.9 kd protein in sec53-act1 intergenic region precursor] [gicfc:12.6] [keggfc:14.2] [sgdfe:1.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG5327	25994007_f3_5	6739	20842	1617	539	YGL160W	310	7.5(10)-32	Saccharomyces cerevisiae	[ui:ygl160w] [pn:similarity to hypothetical protein yhr047c and fre2p;hypothetical 65.8 kd protein in sut1-rek1 intergenic region] [gn:g1837] [gicfc:12.6] [keggfc:14.2] [sgdfe:1.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG2454	6906942_c1_3	6740	20843	1137	379	YJR049C	246	3.1(10)-34	Saccharomyces cerevisiae	[ui:yjr049c] [pn:associated with ferric reductase activity:utr1 protein;unknown transcript 1 protein] [gn:utr1j1655] [gicfc:12.6] [keggfc:14.2] [sgdfe:1.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG5618	24470936_c2_21	6741	20844	1026	342	YJR049C	671	4.7(10)-66	Saccharomyces cerevisiae	[ui:yjr049c] [pn:associated with ferric reductase activity:utr1 protein;unknown transcript 1 protein] [gn:utr1j1655] [gicfc:12.6] [keggfc:14.2] [sgdfe:1.8.1] [db:gic-saccharomyces cerevisiae]

CONTIG1675	32507707_f3_2	6742	20845	915	305	YJR126C	450	7.4(10)-42	Saccharomyces cerevisiae	[ui:yjr126c] [pn:similarity to human prostate-specific membrane antigen and transferrin receptor protein:hypothetical 92.0 kd protein in rps5-zms1 intergenic region] [gn:j2050] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharo
CONTIG2183	10658266_f1_2	6743	20846	1584	528	YJR126C	247	3.8(10)-31	Saccharomyces cerevisiae	[ui:yjr126c] [pn:similarity to human prostate-specific membrane antigen and transferrin receptor protein:hypothetical 92.0 kd protein in rps5-zms1 intergenic region] [gn:j2050] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharo
b2x15488.y	881262_c3_2	6744	20847	276	92	YJR126C	130	1.8(10)-7	Saccharomyces cerevisiae	[ui:yjr126c] [pn:similarity to human prostate-specific membrane antigen and transferrin receptor protein:hypothetical 92.0 kd protein in rps5-zms1 intergenic region] [gn:j2050] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharo
CONTIG3296	978125_c1_5	6745	20848	1023	341	YLL051C	136	5.2(10)-6	Saccharomyces cerevisiae	[ui:yll051c] [pn:strong similarity to ferric reductase fre2p] [gtcf:12.6] [kegfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2351	34553768_c2_6	6746	20849	2178	726	YNR060W	801	7.7(10)-80	Saccharomyces cerevisiae	[ui:ymr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarly to fre1p;hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gcfc:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gc-
CONTIG3089	5906687_c1_3	6747	20850	837	279	YNR060W	348	5.9(10)-31	Saccharomyces cerevisiae	[ui:ymr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarly to fre1p;hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gcfc:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gc-
CONTIG4409	16609568_f1_1	6748	20851	1800	600	YNR060W	628	3.2(10)-73	Saccharomyces cerevisiae	[ui:ymr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarly to fre1p;hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gcfc:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gc-
CONTIG4657	24414812_f1_1	6749	20852	1560	520	YNR060W	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ymr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarly to fre1p;hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gcfc:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gc-

CONTIG4589	23484552_f1_1	6750	20853	1296	432	YNR060W	283	1.2(10)-22	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p: hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gtc-kegfc:14.2]
CONTIG4620	2343803_f1_1	6751	20854	1650	550	YNR060W	705	1.2(10)-69	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p: hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gtc-kegfc:14.2]
CONTIG2018	2401017_f2_1	6752	20855	903	301	YOR381W	415	2.7(10)-38	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1464	6742183_f2_2	6753	20856	822	274	YOR381W	257	3.7(10)-21	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2530	1995906_c2_5	6754	20857	2043	681	YOR381W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4317	1953885_f3_2	6755	20858	2097	699	YOR381W	746	5.2(10)-74	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG5391	12597202_c3_21	6756	20859	1119	373	YOR384W	232	9.6(10)-19	Saccharomyces cerevisiae	[ui:yor384w] [pn:strong similarity to ferric reductase fre2p] [gtcf:12.6] [kegfc:14.2] [sgdfe:1.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG5247	30703938_c2_19	6757	20860	1221	407	YPR129W	200	1.8(10)-31	Saccharomyces cerevisiae	[ui:ypr129w] [pn:suppressor of clathrin deficiency:scd6 protein] [gn:scd6:p9659] [gtcf:12.6] [kegfc:14.2] [sgdfe:8.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG2449	13863760_f3_2	6758	20861	558	186	YLR109W	261	1.3(10)-22	Saccharomyces cerevisiae	[ui:yhr109w] [pn:similarity to c.boiidiu peroxisomal membrane protein 20k a:putative peroxisomal membrane protein] [gn:12916:p9354] [gtcf:12.6] [kegfc:14.2] [sgdfe:9.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG4653	13070413_f3_6	6759	20862	633	211	YLR109W	187	9.0(10)-15	Saccharomyces cerevisiae	[ui:yhr109w] [pn:similarity to c.boiidiu peroxisomal membrane protein 20k a:putative peroxisomal membrane protein] [gn:12916:p9354] [gtcf:12.6] [kegfc:14.2] [sgdfe:9.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5494	14556527_f1_1	6760	20863	738	246	YLR251W	184	2.5(10)-26	Saccharomyces cerevisiae	[ui:yhr251w] [pn:similarity to peroxisomal rat membrane protein pmp22] [gtcf:12.6] [kegfc:14.2] [sgdfe:9.8.0] [db:gic-saccharomyces cerevisiae]



CONTIG5494	23990636_f1_2	6761	20864	675	225	YLR251W	319	9.4(10)-29	Saccharomyces cerevisiae	[ui:ylr251w] [pn:similarity to peroxisomal rat membrane protein pmp22] [gtcf:12.6] [keggfc:14.2] [sgdfe:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG540	23626625_c3_3	6762	20865	483	161	YOL147C	150	7.5(10)-11	Saccharomyces cerevisiae	[ui:vol147c] [pn:peroxisomal membrane protein] [gn:pmp27] [gtcf:12.6] [keggfc:14.2] [sgdfe:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3007	4485902_f1_2	6763	20866	549	183	YDL127W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:ydl127w] [pn:cyclin, g1/s-specific:g1/s-specific cyclin pcl2:cyclin hcs26 homolog] [gn:pcl2:cln4] [gtcf:12.8] [keggfc:13.1] [sgdfe:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4591	4475176_c3_8	6764	20867	1146	382	YDL127W	348	7.9(10)-32	Saccharomyces cerevisiae	[ui:ydl127w] [pn:cyclin, g1/s-specific:g1/s-specific cyclin pcl2:cyclin hcs26 homolog] [gn:pcl2:cln4] [gtcf:12.8] [keggfc:13.1] [sgdfe:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1013	24698791_f2_1	6765	20868	708	236	Q02959	438	7.0(10)-41	Saccharomyces cerevisiae	[gn:hos3:yp116w:ph11w] [sr:baker's yeast] [de:hos3 protein] [sp:q02959] [db:swissprot]
b2x12717.y	10558180_f3_1	6766	20869	528	176	Q02959	451	2.5(10)-42	Saccharomyces cerevisiae	[gn:hos3:yp116w:ph11w] [sr:baker's yeast] [de:hos3 protein] [sp:q02959] [db:swissprot]
CONTIG5811	1273292_f3_16	6767	20870	1326	442	S74213	1059	3.6(10)-107	Methylophilus methylotrophus	[pn:formamidase, a] [gn:fmnd] [ec:3.5.1.49] [db:pir]
b3x16051.y	23562594_c2_3	6768	20871	216	72	S72165	106	8.9(10)-6	Rhizobium leguminosarum	[pn:probable alcohol dehydrogenase] [db:pir]

CONTIG3137	4728300_f3_3	6769	20872	225	75	E69538	92	0.00129	Archaeoglobus fulgidus	[pn:conserved hypothetical transmembrane protein aI2309] [db:pir]
CONTIG4762	22438207_c1_12	6770	20873	420	140	S78075	238	3.6(10)-20	Saccharomyces cerevisiae	[pn:hyphothetical protein yj135w-a] [db:pir] [mp:10r]
CONTIG5765	24489665_f2_6	6771	20874	570	190	S78074	309	1.1(10)-27	Saccharomyces cerevisiae	[pn:hyphothetical protein yk1053c-a] [db:pir] [mp:111]
CONTIG4792	16251002_f1_1	6772	20875	2436	812	S71461	180	3.6(10)-11	Coprinus cinereus	[pn:rad9 protein] [db:pir]
CONTIG4237	954687_c1_5	6773	20876	357	119	JC5710	98	6.2(10)-5	Mus musculus	[pn:rat binding protein-1 interacting protein] [sr:, house mouse] [db:pir]
CONTIG5502	14881512_f1_1	6774	20877	777	259	S71489	321	9.8(10)-29	Rattus norvegicus	[pn:sulfalanine decarboxylase.] [sr:, norway rat] [cc:4.1.1.29] [db:pir]
CONTIG4934	29376628_f1_1	6775	20878	2859	953	AF036485	95	0.07499	no gb taxonomy match	[pn:unknown] [db:genpept-bc] [de:plasmid pnz4000 replication protein (repb2) gene, complete cds; andunknown gene.] [nt:orf2]
CONTIG5610	21679692_f2_4	6776	20879	1047	349	U53868	95	0.16	Clostridium acetobutylicum	[pn:mtlr] [gn:mtlr] [sr:clostridium acetobutylicum strain=dsn 792] [db:genpept-bc] [de:clostridium acetobutylicum mannitol-specific phosphotransferasesystem (pis) system, mtlr, mtlf, and mtd genes, completecds.] [nt:putative p
CONTIG125	627291_f3_1	6777	20880	594	198	AL021287	181	3.2(10)-13	Mycobacterium tuberculosis	[pn:monoxigenase] [gn:mtv012.64c] [db:genpept-bc] [de:mycobacterium tuberculosis sequence v012.] [nt:mtv012.64c, len: 524, probable monoxigenase.]

CONTIG2722	29898518_f1_1	6778	20881	360	120	AL021287	92	0.00129	Mycobacterium tuberculosis	[pn:monooxygenase] [gn:mtv012.64c] [db:genpept-bc1] [de:mycobacterium tuberculosis sequence v012.] [int:mtv012.64c, len: 524, probable monooxygenase,]
CONTIG5776	5179031_c2_28	6779	20882	762	254	AL021287	308	4.4(10)-27	Mycobacterium tuberculosis	[pn:monooxygenase] [gn:mtv012.64c] [db:genpept-bc1] [de:mycobacterium tuberculosis sequence v012.] [int:mtv012.64c, len: 524, probable monooxygenase,]
CONTIG573	35437539_c1_2	6780	20883	1029	343	AL021287	400	2.3(10)-37	Mycobacterium tuberculosis	[pn:monooxygenase] [gn:mtv012.64c] [db:genpept-bc1] [de:mycobacterium tuberculosis sequence v012.] [int:mtv012.64c, len: 524, probable monooxygenase,]
CONTIG5133	11753752_f3_4	6781	20884	984	328	AL021841	224	1.1(10)-18	Mycobacterium tuberculosis	[pn:hypothetical protein mtv016.42] [gn:mtv016.42] [db:genpept-bc1] [de:mycobacterium tuberculosis sequence v016.] [int:mtv016.42, len: 243, unknown but some similarity to]
CONTIG4574	34250002_f1_1	6782	20885	2475	825	AL021942	419	4.5(10)-36	Mycobacterium tuberculosis	[pn:hypothetical protein] [gn:mtv039.22] [db:genpept-bc1] [de:mycobacterium tuberculosis sequence v039.] [int:mtv039.22, len: 877, unknown, contains ps00699]
CONTIG5446	24650037_c1_7	6783	20886	240	80	AF036171	95	0.00062	Dictyostelium discoideum	[pn:homeobox-containing protein] [gn:hbx-2] [db:genpept-inv] [de:dictyostelium discoideum homeobox-containing protein (hbx-2) mrna, partial cds.]

CONTIG2839	3941375_c3_8	6784	20887	1053	351	AF051898	102	0.01499	Dictyostelium discoideum	[pn:coronin binding protein] [gn:db10] [db:genpept-inv] [de:dictyostelium discoideum coronin binding protein (db10) mrna,complete cds.]
b2x13496.x	24117127_c3_2	6785	20888	681	227	Z83109	90	0.51	Caenorhabditis elegans	[pn:f44g3.8] [db:genpept-inv] [de:caenorhabditis elegans cosmid f44g3, complete sequence.]
CONTIG1133	6131312_f3_1	6786	20889	642	214	AF043699	192	7.7(10)-14	Caenorhabditis elegans	[gn:k02f2.3] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid k02f2.] [nt:similar to a human orf (gb:dl3642) and human]
b1x13240.x	24807651_f3_1	6787	20890	732	244	AF043699	271	2.8(10)-22	Caenorhabditis elegans	[gn:k02f2.3] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid k02f2.] [nt:similar to a human orf (gb:dl3642) and human]
b1x13240.y	11765686_c1_1	6788	20891	594	198	AF043699	342	7.7(10)-30	Caenorhabditis elegans	[gn:k02f2.3] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid k02f2.] [nt:similar to a human orf (gb:dl3642) and human]
CONTIG4777	34252143_c3_11	6789	20892	210	70	AL021481	100	0.00021	Caenorhabditis elegans	[pn:y43fab.5] [db:genpept-inv] [de:caenorhabditis elegans cosmid y43fab, complete sequence.]
CONTIG5500	35603436_f1_3	6790	20893	909	303	Z82287	141	3.1(10)-7	Caenorhabditis elegans	[pn:zk550.b] [db:genpept-inv] [de:caenorhabditis elegans cosmid zk550, complete sequence.] [nt:protein predicted using genefinder, preliminary]

CONTIG4756	4022311_c1_10	6791	20894	285	95	Z98269	171	4.5(10)-13	Drosophila melanogaster	[gn:eg.87b1.6] [sr:fruit fly] [db:genpept-iny] [de:drosophila melanogaster cosmid 87b1.]
CONTIG4769	14726437_c2_8	6792	20895	2088	696	AL022018	103	0.07099	Drosophila melanogaster	[gn:eg.8d8.4] [sr:fruit fly] [db:genpept-iny] [de:drosophila melanogaster cosmid 8d8.] [nt:1-evidence=predicted by content;]
CONTIG3480	4453186_f3_2	6793	20896	2217	739	U86010	92	0.87	Drosophila melanogaster	[pn:zinc-finger nuclear protein hindsight] [gn:hindsight] [sr:fruit fly] [db:genpept-iny] [de:drosophila zinc-finger nuclear protein hindsight, complete cds.] [nt:required for germ band retraction during drosophila]
CONTIG4924	24099031_c3_12	6794	20897	930	310	AB006362	1019	6.2(10)-103	Candida albicans	[gn:casin1] [sr:candida albicans dna] [db:genpept-p1n] [de:candida albicans casin1 gene, complete cds.] [nt:similar to sin1 p of s. cerevisiae]
CONTIG5238	34650257_f3_3	6795	20898	1851	617	AB006362	2584	9.0(10)-269	Candida albicans	[gn:casin1] [sr:candida albicans dna] [db:genpept-p1n] [de:candida albicans casin1 gene, complete cds.] [nt:similar to sin1 p of s. cerevisiae]
CONTIG5238	9953800_f3_4	6796	20899	186	62	AB006362	249	7.5(10)-20	Candida albicans	[gn:casin1] [sr:candida albicans dna] [db:genpept-p1n] [de:candida albicans casin1 gene, complete cds.] [nt:similar to sin1 p of s. cerevisiae]
CONTIG4924	31925174_c1_10	6797	20900	1020	340	AB006362	1109	1.8(10)-112	Candida albicans	[gn:casin1] [sr:candida albicans dna] [db:genpept-p1n] [de:candida albicans casin1 gene, complete cds.] [nt:similar to sin1 p of s. cerevisiae]

CONTIG2524	25673907_f2_1	6798	20901	729	243	AB006363	1079	2.7(10)-109	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
CONTIG704	402082_f2_1	6799	20902	282	94	AB006363	250	4.2(10)-20	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
CONTIG704	3131388_f3_2	6800	20903	1197	399	AB006363	1548	5.5(10)-159	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
b9x13n67.x	29315663_c3_3	6801	20904	696	232	AB006363	922	1.2(10)-92	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
CONTIG553	25587591_f2_2	6802	20905	195	65	AB010636	139	4.9(10)-9	Candida parapsilosis	[pn:sadh] [gn:sadh] [sr:candida parapsilosis dna] [db:genpept-pln] [de:candida parapsilosis gene for sadh, complete cds.]
CONTIG5661	22437512_c3_15	6803	20906	1146	382	AB010636	1187	9.8(10)-121	Candida parapsilosis	[pn:sadh] [gn:sadh] [sr:candida parapsilosis dna] [db:genpept-pln] [de:candida parapsilosis gene for sadh, complete cds.]
CONTIG3416	157892_f2_3	6804	20907	1095	365	AF013273	1664	1.8(10)-170	Candida albicans	[pn:histidine kinase 1] [db:genpept-pln] [de:candida albicans histidine kinase 1 gene, complete cds.] [nt:two-component phopho-relay protein homolg; cank1]

CONTIG4713	5079500_f2_1	6805	20908	3003	1001	AF013273	4730	0	Candida albicans	[pn:histidine kinase I] [db:genpept-pln] [de:candida albicans histidine kinase I gene, complete cds.] [nt:two-component phospho-relay protein homolog; cahk1]
CONTIG4845	9821038_c1_4	6806	20909	3009	1003	AF013273	5056	0	Candida albicans	[pn:histidine kinase I] [db:genpept-pln] [de:candida albicans histidine kinase I gene, complete cds.] [nt:two-component phospho-relay protein homolog; cahk1]
CONTIG1906	24422265_c2_4	6807	20910	672	224	AF038152	408	1.1(10)-52	Mycosphaerella graminicola	[pn:4-hydroxyphenylpyruvate dioxygenase] [gn:hppd] [fn:converts 4-hydroxyphenylpyruvate to] [db:genpept-pln] [ec:1.13.11.27] [de:mycosphaerella graminicola 4-hydroxyphenylpyruvate dioxygenase(hppd) gene, complete cds.] [nt:tyrosine ca
CONTIG5194	835177_f2_2	6808	20911	834	278	AF038154	1171	4.9(10)-119	Candida albicans	[pn:14-3-3 protein] [gn:bmh] [db:genpept-pln] [de:candida albicans 14-3-3 protein (bmh) gene, complete cds.]
CONTIG5598	34157200_f3_15	6809	20912	471	157	AF042334	151	2.7(10)-10	Arabidopsis thaliana	[pn:jab1] [gn:jab1] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana jab1 (jab1) mma, complete cds.] [nt:similar to jun activation domain binding protein]
CONTIG5598	26272312_f2_9	6810	20913	918	306	AF042334	410	2.1(10)-38	Arabidopsis thaliana	[pn:jab1] [gn:jab1] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana jab1 (jab1) mma, complete cds.] [nt:similar to jun activation domain binding protein]

CONTIG128	25407686_c3_1	6811	20914	522	174	AF043330	150	4.5(10)-10	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap8] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap8) gene, completecds.] [nt:sap8p]
CONTIG776	4798431_c2_1	6812	20915	666	222	AF043330	915	6.5(10)-92	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap8] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap8) gene, completecds.] [nt:sap8p]
CONTIG4521	9843750_c3_5	6813	20916	1713	571	AF043331	2215	1.1(10)-229	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap9] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap9) gene, completecds.] [nt:sap9p]
b3x13783.y	35803410_f3_1	6814	20917	366	122	AF043331	101	0.00013	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap9] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap9) gene, completecds.] [nt:sap9p]
CONTIG4761	4507692_c3_8	6815	20918	942	314	AF045774	1603	8.0(10)-165	Candida albicans	[pn:sir2] [gn:sir2] [db:genpept-pln] [de:candida albicans sir2 (sir2) gene, complete cds.] [nt:similar to saccharomyces cerevisiae sir2]
b2x15833.x	2390833_f2_1	6816	20919	504	168	AF045774	524	1.8(10)-50	Candida albicans	[pn:sir2] [gn:sir2] [db:genpept-pln] [de:candida albicans sir2 (sir2) gene, complete cds.] [nt:similar to saccharomyces cerevisiae sir2]
CONTIG1957	10945312_f2_1	6817	20920	585	195	AF049069	622	7.2(10)-61	Pinus radiata	[gn:pre87] [sr:monterey pine] [db:genpept-pln] [de:pinus radiata pre87 mrna, complete cds.]



CONTIG4287	33360900_c1_8	6818	20921	1497	499	AJ223459	360	4.5(10)-31	Emericella nidulans	[pn:prna protein] [gn:prna] [ln:transcriptional activator] [db:genpept-p1n] [de:aspergillus nidulans prna gene.]
CONTIG1313	175765_c2_3	6819	20922	771	257	AJ223508	435	5.7(10)-40	Arabidopsis thaliana	[pn:zwille protein] [gn:zwille] [sr:thale cress] [db:genpept-p1n] [de:arabidopsis thaliana mrna for zwille protein.]
b2x14678.y	25651050_f2_1	6820	20923	855	285	AC002334	96	0.11	Arabidopsis thaliana	[pn:similar to disease resistance protein] [gn:f25i18.21] [sr:thale cress] [db:genpept-p1n] [de:arabidopsis thaliana chromosome ii bac f25i18 genomic sequence,complete sequence.]
CONTIG4766	16021900_c3_7	6821	20924	849	283	AC002340	242	4.4(10)-20	Arabidopsis thaliana	[gn:t1j7.11] [sr:thale cress] [db:genpept-p1n] [de:arabidopsis thaliana chromosome ii bac t1j7 genomic sequence,complete sequence.] [nt:hypothetical protein]
CONTIG2283	36117000_c3_4	6822	20925	1002	334	AC002561	571	7.7(10)-54	Arabidopsis thaliana	[pn:putative atp-dependent rna helicase] [gn:t24p15.18] [sr:thale cress] [db:genpept-p1n] [de:arabidopsis thaliana chromosome ii bac t24p15 genomic sequence,complete sequence.]
CONTIG4297	22710042_c3_7	6823	20926	1017	339	AC003033	103	0.029	Arabidopsis thaliana	[pn:putative disease resistance protein (cf-2.2)] [gn:t21114.4] [sr:thale cress] [db:genpept-p1n] [de:arabidopsis thaliana chromosome ii bac t21114 genomic sequence,complete sequence.]

CONTIG4144	822026_f3_3	6824	20927	873	291	AC003673	201	4.4(10)-23	Arabidopsis thaliana	[gn:f19124.4] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana chromosome ii bac f19124 genomic sequence,complete sequence.] [nt:unknown protein]
CONTIG2776	522953_c2_7	6825	20928	1632	544	AL021768	94	0.0057	Arabidopsis thaliana	[pn:resistance protein rpp5 - like] [gn:f24j7.80] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana dna chromosome 4, bac clone f24j7 (essaiiproject).] [nt:similarity to downy mildew resistance protein rpp5.]
CONTIG4818	392055_c2_8	6826	20929	972	324	AL021890	99	4.4(10)-7	Arabidopsis thaliana	[pn:putative protein] [gn:t805.20] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana dna chromosome 4, bac clone t805 (essaiiproject).] [nt:similarity to nadh dehydrogenase chain 4.]
CONTIG3745	26572343_c3_9	6827	20930	222	74	Y17007	221	3.7(10)-17	Candida albicans	[pn:piruvate decarboxylase] [gn:pdcc2] [db:genpept-pln] [de:candida albicans pdcc2 gene.]
CONTIG3745	36365936_c3_8	6828	20931	1980	660	Y17007	3094	0	Candida albicans	[pn:piruvate decarboxylase] [gn:pdcc2] [db:genpept-pln] [de:candida albicans pdcc2 gene.]
CONTIG3703	7063438_c1_6	6829	20932	477	159	AJ222805	637	1.8(10)-62	Candida albicans	[pn:srp54 protein] [gn:srp54] [fn:54 kd subunit of the signal recognition] [db:genpept-pln] [de:candida albicans mrna for srp54 protein homologue.]
CONTIG4262	25445438_f1_2	6830	20933	936	312	U84588	97	0.00016	Candida albicans	[db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]

CONTIG4297	3914061_c3_6	6831	20934	837	279	U84588	91	0.00063	Candida albicans	[db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]
CONTIG4915	23609406_c2_9	6832	20935	1185	395	U84588	122	4.5(10)-7	Candida albicans	[db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]
CONTIG5656	9820801_f2_8	6833	20936	1734	578	U84588	403	1.2(10)-37	Candida albicans	[db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]
CONTIG5656	3163432_c1_15	6834	20937	585	195	U84588	993	3.5(10)-100	Candida albicans	[pn:dihydrofolate reductase] [gn:dfr1] [db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.]
CONTIG5021	15891378_c3_12	6835	20938	1068	356	U96385	97	0.014	Penicillium chrysogenum	[pn:gata transcription factor] [gn:nreb] [db:genpept-pln] [de:penicillium chrysogenum gata transcription factor (nreb) gene, complete cds.] [nt:nreb; nitrogen regulatory gata factor]
CONTIG5116	16605035_c1_7	6836	20939	2448	816	Z97209	100	0.035	Schizosaccharomyces pombe	[pn:thyothetical protein] [gn:spac19g12.17c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c19g12.] [nt:spac19g12.17c, partial; unknown, len:223aa, similar]

CONTIG3661	4381317_f2_1	6837	20940	354	118	AL009227	104	5.7(10)-6	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac27d7.04] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c27d7.] [nt:spac27d7.04, unknown, len:96aa, similar eg. to]
CONTIG2520	24020463_c3_3	6838	20941	873	291	AL021817	105	0.00169	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spac8e11.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c8e11.] [nt:spac8e11.05c, unknown, len:338aa]
CONTIG4146	19923386_f1_1	6839	20942	735	245	AL022117	642	5.5(10)-63	Schizosaccharo myces pombe	[pn:putative o-methyltransferase] [gn:spbc119.03] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c119.] [nt:spbc119.03, putative o- methyltransferase.]
CONTIG5242	26375057_f1_1	6840	20943	729	243	AL022305	464	4.0(10)-44	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spbc14c8.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c14c8.] [nt:spbc14c8.06, unknown, len:377aa, similar eg. to h.]
CONTIG2785	14242216_c2_4	6841	20944	1191	397	AL022305	330	1.0(10)-39	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spbc14c8.14c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c14c8.] [nt:spbc14c8.14c, unknown (appears frame-shifted as)]

CONTIG4913	214583_c2_9	6842	20945	663	221	AL021748	247	6.2(10)-21	Schizosaccharo myces pombe	[pn:adenosine deaminase] [gn:spbc16a3.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16a3.] [nt:spbc16a3.06, probable adenosine deaminase; contains]
CONTIG454	23625277_c3_4	6843	20946	759	253	AL021748	139	1.5(10)-6	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spbc16a3.11] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16a3.] [nt:spbc16a3.11, unknown, len:872aa, similar eg. to {}]
CONTIG1614	23867677_c1_2	6844	20947	1224	408	AL022104	240	1.2(10)-22	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spbc16h5.12c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16h5.] [nt:spbc16h5.12c, unknown; (possible alternative n)]
CONTIG1278	10756307_c2_4	6845	20948	462	154	AL022304	189	1.7(10)-14	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spbc18h10.06c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c18h10.] [nt:spbc18h10.06c, unknown, len:357aa, similar eg. to {}]
CONTIG5247	4938912_f1_3	6846	20949	801	267	AL021839	483	3.8(10)-46	Schizosaccharo myces pombe	[pn:hypothetical protein] [gn:spbc19g7.16] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c19g7.] [nt:spbc19g7.16, unknown, len:429aa, similar eg. to s.]

CONTIG5120	22063431_f1_1	6847	20950	1344	448	AL021746	242	3.7(10)-27	Schizosaccharo myces pombe	[pn:hyothetical anaphase promoting factor] [gn:spbc1e8.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c1e8.] [nt:spbc1e8.06, possible anaphase promoting factor]
CONTIG772	24304652_f2_1	6848	20951	714	238	AL021747	276	1.0(10)-30	Schizosaccharo myces pombe	[pn:hyothetical mitotic feedback control protein] [gn:spbc20f10.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c20f10.] [nt:spbc20f10.06, putative mitotic feedback control]
CONTIG4577	9777127_f1_1	6849	20952	1425	475	AL021747	102	0.00719	Schizosaccharo myces pombe	[pn:hyothetical protein] [gn:spbc20f10.10] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c20f10.] [nt:spbc20f10.10, unknown, len:243aa, similar eg. to]
b2x14795.y	5883505_c1_3	6850	20953	429	143	AL021816	137	7.4(10)-9	Schizosaccharo myces pombe	[pn:hyothetical protein] [gn:spbc24e9.11c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c24e9.] [nt:spbc24e9.11c, probable transporter, len:322aa,]
CONTIG5236	34037817_f1_4	6851	20954	744	248	AL021816	331	5.0(10)-30	Schizosaccharo myces pombe	[pn:hyothetical protein] [gn:spbc24e9.14c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c24e9.] [nt:spbc24e9.14c, unknown, len:238aa, similar eg. to]

CONTIG5818	24509812_c2_42	6852	20955	1851	617	AL0222299	835	2.0(10)-83	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spbc29a3.06] [sr:ffission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c29a3.] [nt:spbc29a3.06, unknown, len:556aa, similar eg. to]
CONTIG3167	23984817_f2_3	6853	20956	1245	415	AL0222299	118	7.9(10)-8	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spbc29a3.08] [sr:ffission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c29a3.] [nt:spbc29a3.08, unknown; len:199aa, some silarity at]
bix13326.y	10241630_f2_1	6854	20957	285	95	AL022103	210	3.2(10)-17	Schizosaccharo myces pombe	[pn:putative protein transport protein] [gn:spbc2g2.03c] [sr:ffission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c2g2.] [nt:spbc2g2.03c, putative protein transport protein.]
CONTIG5458	23437627_c1_10	6855	20958	924	308	AL022103	278	2.1(10)-24	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spbc2g2.15c] [sr:ffission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c2g2.] [nt:spbc2g2.15c, unknown, len:218aa, similar eg. to m.]
CONTIG2557	15087583_f2_2	6856	20959	276	92	AL022071	92	0.00209	Schizosaccharo myces pombe	[pn:hyposhethcal protein] [gn:spbc354.05c] [sr:ffission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c354.] [nt:spbc354.05c, unknown, len:793aa, similar eg. to the]

CONTIG1612	36222075_f2_1	6857	20960	1023	341	AL022244	843	2.7(10)-84	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spbc3b8.07c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c3b8.] [nt:spbc3b8.07c, unknown (putative transmembrane).]
CONTIG5039	33260311_f1_1	6858	20961	201	67	AL022070	125	3.3(10)-8	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spbc3b9.12] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c3b9.] [nt:spbc3b9.12, unknown, len:132aa, similar eg. to s.]
CONTIG3249	4894061_c3_5	6859	20962	540	180	AL021730	90	0.14999	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spbc4c3.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c4c3.] [nt:spbc4c3.06, unknown, len:818aa, similar eg. to .]
CONTIG2788	968791_f3_3	6860	20963	876	292	AL021730	183	4.9(10)-19	Schizosaccharo myces pombe	[pn:hyprothetical protein] [gn:spbc4c3.07] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c4c3.] [nt:spbc4c3.07, unknown, len:302aa, similar eg. to a.]
CONTIG4780	22299050_c1_7	6861	20964	246	82	U75447	94	0.0016	Yarrowia lipolytica	[pn:p-type calcium atpase] [gn:scal] [db:genpept-pln] [de:yarrowia lipolytica p-type calcium atpase (scal) gene, completecds.] [nt:secretory calcium atpase]



CONTIG5097	19573500_f1_2	6862	20965	504	168	AB008430	114	1.3(10)-5	Homo sapiens	[pn:cdep] [fr:rho guanine nucleotide exchange factor] [sr:homo sapiens embryo cartilage chondrocyte cdna to mma] [db:genpept-pri2] [de:homo sapiens mma for cdep, complete cds.] [nt:band 4.1 superfamily]
CONTIG3365	6651700_c3_3	6863	20966	810	270	AB011145	135	1.8(10)-6	Homo sapiens	[pn:kiaa0573 protein] [gn:kiaa0573] [sr:homo sapiens male brain cdna to mma, clone_lib:pbbluecriptii s] [db:genpept-pri2] [de:homo sapiens mma for kiaa0573 protein, partial cds.]
CONTIG3647	30292180_f1_3	6864	20967	1857	619	AB011157	350	1.2(10)-31	Homo sapiens	[pn:kiaa0585 protein] [gn:kiaa0585] [sr:homo sapiens male brain cdna to mma, clone_lib:pbbluecriptii s] [db:genpept-pri2] [de:homo sapiens mma for kiaa0585 protein, partial cds.]
CONTIG1181	21979002_c1_1	6865	20968	525	175	AF042384	419	2.3(10)-39	Homo sapiens	[pn:bc-2 protein] [sr:human] [db:genpept-pri2] [de:homo sapiens bc-2 protein mma, complete cds.] [nt:p32; putative breast adenocarcinoma marker]
CONTIG5594	23829663_c3_19	6866	20969	939	313	AF042384	157	3.2(10)-10	Homo sapiens	[pn:bc-2 protein] [sr:human] [db:genpept-pri2] [de:homo sapiens bc-2 protein mma, complete cds.] [nt:p32; putative breast adenocarcinoma marker]

b9x10y60.x	29454517_c1_3	6867	20970	621	207	AF047599	128	4.0(10)-6	Homo sapiens	[pn:origin recognition complex subunit 5] [gn:orc5] [sr:human] [db:genpept-pri2] [de:homo sapiens origin recognition complex subunit 5 (orc5) mma,complete cds.] [nt:orc5p]
CONTIG2379	2850811_f2_3	6868	20971	591	197	AF048977	162	7.2(10)-11	Homo sapiens	[pn:ser/arg-related nuclear matrix protein] [gn:srm160] [fn:splicing factor] [sr:human] [db:genpept-pri2] [de:homo sapiens ser/arg-related nuclear matrix protein (srm160) mma,complete cds.] [nt:160 kda]
CONTIG5202	1412961_c2_7	6869	20972	1761	587	U60337	486	1.2(10)-45	Homo sapiens	[pn:beta-mannosidase] [sr:human] [db:genpept-pri2] [de:homo sapiens beta-mannosidase mma, complete cds.] [nt:acid hydrolase; glycosyl hydrolase; lysosomal]
CONTIG5765	13832755_f2_7	6870	20973	726	242	U61837	112	2.7(10)-6	Homo sapiens	[pn:putative cyclin g1 interacting protein] [sr:human] [db:genpept-pri2] [de:homo sapiens putative cyclin g1 interacting protein mma, completecds.]
CONTIG4557	21993765_c1_6	6871	20974	666	222	Y15173	93	0.039	no gb taxonomy match	[gn:e2] [or:human papillomavirus type 75] [db:genpept-vrt] [de:human papillomavirus type 75 c6, c7, c1, c2, c4, 12, and 11 genes.] [nt:putative]
CONTIG1609	24500031_c2_5	6872	20975	1056	352	Y08997	766	3.2(10)-75	Xenopus laevis	[pn:146kda nuclear protein] [sr:african clawed frog] [db:genpept-vrt] [de:xenopus laevis mma for 146 kda nuclear protein.]

CONTIG5304	16800013_f3_5	6873	20976	360	120	CONTIG74 ID	289	2.1(10)-26	Streptococcus pneumoniae	[pn:nuclear pore complex glycoprotein p62] [sr:oncorhynchus mykiss cdna to mrna, clone:povc- ap-75] [db:genpept-vrt] [de:oncorhynchus mykiss mrna for nuclear pore complex glycoprotein p62,complete cds.]
CONTIG5340	23868830_c3_9	6874	20977	963	321	CONTIG40 OC	114	8.5(10)-6	Enterococcus faecium	[ui:spovc] [pn:hypothetical protein:probable peptidyl-trna hydrolase:stage v sporulation protein c] [gn:pth] [gicfc:10.6] [ec:3.1.1.29] [kegfc:14.1] [bsorfic:6.2.1] [db:gtc-bacillus subtilis]
CONTIG5184	25516263_f1_2	6875	20978	603	201	CONTIG42 2C	122	1.5(10)-7	Enterococcus faecium	[gn:a540] [or:paramecium bursaria chlorella virus 1] [db:genpept-vrt] [de:paramecium bursaria chlorella virus 1 genome, complete sequence.]
CONTIG5648	4958425_c1_13	6876	20979	360	120	CONTIG42 2C	91	0.00032	Enterococcus faecium	[gn:a540] [or:paramecium bursaria chlorella virus 1] [db:genpept-vrt] [de:paramecium bursaria chlorella virus 1 genome, complete sequence.]
CONTIG5414	14664636_f1_1	6877	20980	2652	884	CONTIG42 7C	95	0.049	Enterococcus faecium	[pn:b. burgdorferi predicted coding region bb0039] [gn:bb0039] [sr:lyme disease spirochete] [db:genbank] [de:borrelia burgdorferi (section 3 of 70) of the complete genome.] [nt:hypothetical protein; identified by genemark;]

CONTIG5168	799133_c1_10	6878	20981	1188	396	CONTIG49 1C	93	0.034	Enterococcus faecium	[ui:treal] [pn:trehalose-6-phosphate hydrolase] [gn:trecl] [gctc:1.4.7.2] [ec:3.2.1.93] [keggfc:7.1] [bsorffc:2.1.1] [db:gtc-bacillus subtilis]
CONTIG1818	12554653_f2_3	6879	20982	213	71	CONTIG51 4C	105	6.5(10)-7	Enterococcus faecium	or:saccharomyces cerevisiae pn:unknown gn:internalorf g1669 le:6964 re:7365 di:direct sr:baker's yeast
CONTIG2704	1416683_c2_6	6880	20983	1047	349	CONTIG18 7C	111	0.00081	Acinetobacter baumannii	[ui:yb208c] [pn:urea amidolyase] [gn:dur1.2] [gctc:2.6.4.1:5.3] [keggfc:14.2] [sgdfc:1.1.4.1.2.1:1.3.1] [db:gtc- saccharomyces cerevisiae]
CONTIG3210	5314142_f3_3	6881	20984	507	169	CONTIG18 8C	102	2.0(10)-5	Acinetobacter baumannii	[ui:inj0304] [pn:ferrityochrome binding protein:dbp:hypothetical protein] [gctc:12.5] [keggfc:14.2] [tigrfc:13.5] [db:gtc-methanococcus jannaschii]
CONTIG2059	6542500_c2_4	6882	20985	519	173	CONTIG20 3C	95	9.8(10)-6	Acinetobacter baumannii	[ui:b0454] [pn:hypothetical protein:hypothetical 14.4 kd protein in tesb-tha intergenic region] [gn:ybaz] [gctc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc- escherichia coli]
CONTIG5811	22783_c1_24	6883	20986	1098	366	CONTIG21 0C	93	0.01099	Acinetobacter baumannii	esterase (ec 3.1.1.-) - pseudomonas putida this enzyme catalyzes the hydrolysis of ester bonds and are found widely in animals, plants and microorganisms. this enzyme is useful for transesterification, synthesis of esters, and resolution of racemic mixt

CONTIG2940	29303436_f1_2	6884	20987	204	68	CONTIG22 0C	91	0.00022	Acinetobacter baumannii	[ui:b2156] [pn:lysine-specific permease] [gn:lysp:cadrl [gtcf:12.1] [keggfc:14.2] [rileyfc:4.1.1] [db:glc-escherichia coli]
CONTIG33	10314008_c3_2	6885	20988	687	229	CONTIG22 3C	92	0.01799	Acinetobacter baumannii	[ui:mg244] [pn:rep helicase, single- stranded dna-dependent atpase:rep:probable dna helicase] [gtcf:9.6:10.8] [ec:3.6.1.-] [keggfc:9.7] [tgrfc:10.2] [db:glc- mycoplasma genitalium]
CONTIG2262	33990932_c2_4	6886	20989	309	103	CONTIG13 8C	138	4.5(10)-10	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG1833	10175182_c2_3	6887	20990	282	94	CONTIG28 4C	121	2.2(10)-8	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG4031	20839217_c1_3	6888	20991	249	83	CONTIG33 2C	124	8.6(10)-8	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
b9x10g13.y	4897052_f1_1	6889	20992	255	85	CONTIG35 1C	140	1.3(10)-10	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG1078	25593802_f3_2	6890	20993	348	116	CONTIG35 8C	93	2.7(10)-5	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG3119	6725307_c1_4	6891	20994	222	74	CONTIG35 8C	115	8.0(10)-8	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG3803	24473433_f3_4	6892	20995	345	115	CONTIG35 8C	144	4.7(10)-11	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG5220	11975300_f2_2	6893	20996	216	72	CONTIG35 8C	95	1.6(10)-5	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG4957	19704411_f2_4	6894	20997	384	128	CONTIG36 2C	97	6.5(10)-5	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG4068	22314540_f1_1	6895	20998	447	149	CONTIG48 9	98	0.00084	Enterobacter cloacae	RANGE ON: [E:cloacae, GTC contig, rel. 2.0]
CONTIG4525	4415882_f3_3	6896	20999	570	190	Contig088 H	97	0.00029	Clostridium acetobutylicum	or:borrelia burgdorferi gn:orfa le:713 re:1801 di:direct sr:lyme disease spirochete

CONTIG5121	4500063_f2_2	6897	21000	1497	499	Contig107 H	91	0.027	Clostridium acetobutylicum	[ui:b4043] [pn:lexa:lexa repressor] [gn:lexa:extra:spr:isl:umua] [gtcf:10.2] [ec:3.4.21.88] [keggfc:14.1] [rileyfc:2.0.0] [db:gtc- escherichia coli]
CONTIG775	14554762_f3_2	6898	21001	357	119	Contig133 H	92	0.00013	Clostridium acetobutylicum	[ui:yxio] [pn:hypothetical protein:hypothetical 47.3 kd protein in wapa-licet intergenic region] [gn:s3ar] [gtcf:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG824	9773431_f2_1	6899	21002	555	185	Contig144 H	97	0.0035	Clostridium acetobutylicum	[ui:rmh172] [pn:conserved protein] [gtcf:14.1:14.2] [keggfc:14.2] [genomfc:14.2] [db:gtc- methanobacterium thermoautotrophicum]
CONTIG5529	16697933_f2_5	6900	21003	183	61	Contig155 H	92	1.5(10)-5	Clostridium acetobutylicum	Hypothetical protein
CONTIG5355	14585016_c1_7	6901	21004	528	176	Contig155 H	119	2.1(10)-8	Clostridium acetobutylicum	Hypothetical protein
b9x11k74.x	24651557_f3_1	6902	21005	495	165	Contig164 H	98	0.00259	Clostridium acetobutylicum	[ui:addd] [pn:atp-dependent deoxyribonuclease:subunit a:atp- dependent nuclease subunit a] [gn:rece5] [gtcf:10.10] [keggfc:14.2] [bsorffc:4.1.2] [db:gtc-bacillus subtilis]
CONTIG2868	21562643_f1_1	6903	21006	1227	409	Contig215 H	100	0.0054	Clostridium acetobutylicum	Hypothetical protein

CONTIG1221	447882_f2_1	6904	21007	1236	412	Contig215 H	115	0.00016	Clostridium acetobutylicum	[ui:ybbd] [pn:hypothetical protein:hyprothetical 70.6 kd protein in feua 5' region precursor:orf1] [gn:yzba] [gcf:1.6.5.13.6.5.7.2.14.1] [ec:3.2.1.21] [kegfc:1.6.5.13.6.5.7.1] [bsorfc:8.1.1] [db:gfc-bacillus subtilis]
CONTIG5230	15814030_f2_9	6905	21008	291	97	Contig227 H	92	3.7(10)-5	Clostridium acetobutylicum	or:mycobacterium tuberculosis pn:unknown protein le:242 re:769 di:complement sr:mycobacterium tuberculosis (strain erdman) dna nt:orf f175; putative
CONTIG4630	24414063_f3_4	6906	21009	2046	682	Contig244 H	92	0.12	Clostridium acetobutylicum	or:bacteroides ovatus pn:arabinoxidase gn:asdi ec:3.2.1.55 le:110 re:2092 di:direct
CONTIG10	22300262_f3_2	6907	21010	213	71					
CONTIG100	5347840_c1_2	6908	21011	186	62					
CONTIG1001	23601510_f2_1	6909	21012	300	100					
CONTIG1002	26457258_f1_1	6910	21013	546	182					
CONTIG1002	26203425_c2_3	6911	21014	186	62					
CONTIG1004	5942800_f3_1	6912	21015	225	75					
CONTIG1008	21538911_c3_3	6913	21016	234	78					
CONTIG101	3180311_f1_1	6914	21017	651	217					
CONTIG101	16132215_f3_7	6915	21018	462	154					
CONTIG1010	10578905_c2_5	6916	21019	444	148					
CONTIG1016	24255251_f3_2	6917	21020	243	81					
CONTIG1017	31814567_c2_2	6918	21021	519	173					
CONTIG1018	34100952_f3_1	6919	21022	183	61					
CONTIG1018	4095275_c3_3	6920	21023	684	228					
CONTIG1019	24226451_c2_2	6921	21024	198	66					
CONTIG102	5859375_c1_5	6922	21025	201	67					
CONTIG102	11718750_c3_7	6923	21026	204	68					

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CONTIGI066	796886_f1_1	6957	21060	303	101
CONTIGI066	24017516_c1_3	6958	21061	255	85
CONTIGI068	4089137_f2_1	6959	21062	297	99
CONTIGI069	31557_f3_2	6960	21063	264	88
CONTIGI070	23439058_f2_3	6961	21064	243	81
CONTIGI071	29322706_f3_1	6962	21065	516	172
CONTIGI073	48588_f3_2	6963	21066	213	71
CONTIGI074	16022156_c1_3	6964	21067	1017	339
CONTIGI079	4687760_f2_3	6965	21068	318	106
CONTIGI080	4085885_f2_1	6966	21069	594	198
CONTIGI084	6103508_f3_1	6967	21070	879	293
CONTIGI089	865699_c1_4	6968	21071	312	104
CONTIGI089	21507676_c3_5	6969	21072	942	314
CONTIGI09	1968876_f1_1	6970	21073	210	70
CONTIGI09	4882186_f1_2	6971	21074	231	77
CONTIGI09	16585287_c2_3	6972	21075	321	107
CONTIGI091	26832260_c2_5	6973	21076	183	61
CONTIGI092	19938901_f3_3	6974	21077	897	299
CONTIGI092	22479188_c2_4	6975	21078	222	74
CONTIGI093	26620877_f2_2	6976	21079	198	66
CONTIGI093	22460937_f2_3	6977	21080	243	81
CONTIGI094	23446900_f1_1	6978	21081	375	125
CONTIGI095	5_f2_4	6979	21082	345	115
CONTIGI095	3994127_c1_6	6980	21083	210	70
CONTIGI096	26225437_f2_1	6981	21084	231	77
CONTIGI097	10720300_f3_1	6982	21085	282	94
CONTIGI098	5908140_f1_1	6983	21086	297	99
CONTIGI098	11884802_c1_4	6984	21087	186	62
CONTIGI099	21742762_f1_1	6985	21088	315	105
CONTIGI099	9782531_c3_2	6986	21089	321	107
CONTIGI102	25672206_f1_1	6987	21090	372	124
CONTIGI102	30250831_f3_2	6988	21091	189	63
CONTIGI107	3132125_f1_2	6989	21092	186	62

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CONTIGI218	10360938_c2_6	7056	21159	438	146															
CONTIGI222	24320282_c2_5	7057	21160	213	71															
CONTIGI223	20112762_f2_1	7058	21161	198	66															
CONTIGI223	31266525_c1_2	7059	21162	186	62															
CONTIGI224	22845635_c1_2	7060	21163	426	142															
CONTIGI227	24256910_c2_3	7061	21164	258	86															
CONTIGI228	5164062_f2_1	7062	21165	873	291															
CONTIGI228	604125_f3_2	7063	21166	246	82															
CONTIGI23	13851587_c2_4	7064	21167	333	111															
CONTIGI232	24797760_f3_1	7065	21168	183	61															
CONTIGI233	22267035_f1_1	7066	21169	1005	335															
CONTIGI233	3960782_f2_2	7067	21170	441	147															
CONTIGI234	12925900_f2_1	7068	21171	357	119															
CONTIGI235	25448513_f3_2	7069	21172	189	63															
CONTIGI235	9957312_f3_4	7070	21173	198	66															
CONTIGI236	34023312_f1_1	7071	21174	198	66															
CONTIGI237	36611640_c3_3	7072	21175	906	302															
CONTIGI238	19792250_f1_1	7073	21176	216	72															
CONTIGI238	1370337_f3_2	7074	21177	183	61															
CONTIGI238	20345086_c1_3	7075	21178	213	71															
CONTIGI238	22767057_c1_4	7076	21179	291	97															
CONTIGI239	12350312_f2_1	7077	21180	816	272															
CONTIGI24	9806262_c2_3	7078	21181	288	96															
CONTIGI241	6820432_f1_1	7079	21182	234	78															
CONTIGI241	12298438_c2_2	7080	21183	738	246															
CONTIGI244	1228160_f1_1	7081	21184	228	76															
CONTIGI244	976418_f3_3	7082	21185	192	64															
CONTIGI245	194075_f3_2	7083	21186	348	116															
CONTIGI248	14563912_f3_2	7084	21187	240	80															
CONTIGI253	26350002_f3_2	7085	21188	186	62															
CONTIGI254	16594050_f1_1	7086	21189	303	101															
CONTIGI255	29568785_f2_1	7087	21190	255	85															
CONTIGI258	32157802_c3_4	7088	21191	186	62															

[illegible]

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CONTIGI382	656327_f3_3	7188	21291	432	144
CONTIGI383	2006928_f3_1	7189	21292	240	80
CONTIGI383	4892250_f3_2	7190	21293	927	309
CONTIGI383	3131301_c3_4	7191	21294	291	97
CONTIGI384	26573312_c3_4	7192	21295	1059	353
CONTIGI385	3234657_f2_2	7193	21296	186	62
CONTIGI385	24430192_c1_4	7194	21297	216	72
CONTIGI389	26807790_c1_1	7195	21298	741	247
CONTIGI389	23868930_c2_2	7196	21299	183	61
CONTIGI39	10207317_f3_2	7197	21300	204	68
CONTIGI391	116250_c1_1	7198	21301	198	66
CONTIGI391	20523263_c2_4	7199	21302	198	66
CONTIGI394	78188_f2_1	7200	21303	288	96
CONTIGI395	24272287_f1_1	7201	21304	279	93
CONTIGI397	7033383_c2_1	7202	21305	1140	380
CONTIGI4	24342200_f2_2	7203	21306	222	74
CONTIGI400	32612677_f1_1	7204	21307	225	75
CONTIGI401	11110766_c2_2	7205	21308	228	76
CONTIGI402	34422253_c3_5	7206	21309	1008	336
CONTIGI403	22067317_f1_1	7207	21310	225	75
CONTIGI403	16408375_c3_6	7208	21311	201	67
CONTIGI404	23617127_c2_4	7209	21312	183	61
CONTIGI404	35331637_c2_5	7210	21313	201	67
CONTIGI404	19562802_c3_6	7211	21314	657	219
CONTIGI405	2677343_f2_1	7212	21315	507	169
CONTIGI406	10814177_f1_1	7213	21316	243	81
CONTIGI406	2739002_c1_3	7214	21317	294	98
CONTIGI407	10677165_f1_2	7215	21318	459	153
CONTIGI408	10439750_f2_4	7216	21319	324	108
CONTIGI41	11500_f1_1	7217	21320	261	87
CONTIGI41	9946002_f1_2	7218	21321	216	72
CONTIGI410	267953_f1_1	7219	21322	882	294
CONTIGI415	3947127_c2_3	7220	21323	1275	425



CONTIGI418	19813138_f3_2	7221	21324	354	118
CONTIGI418	29961635_c1_3	7222	21325	282	94
CONTIGI418	5274132_c2_4	7223	21326	231	77
CONTIGI419	4395287_f1_1	7224	21327	210	70
CONTIGI419	13781556_f3_2	7225	21328	228	76
CONTIGI421	9814066_c2_1	7226	21329	1032	344
CONTIGI423	34484753_c2_1	7227	21330	336	112
CONTIGI425	26376627_c3_3	7228	21331	204	68
CONTIGI428	267131_f1_1	7229	21332	225	75
CONTIGI428	35366563_c2_2	7230	21333	183	61
CONTIGI429	4882785_f2_1	7231	21334	732	244
CONTIGI434	24272161_f3_2	7232	21335	201	67
CONTIGI437	31337752_f1_2	7233	21336	345	115
CONTIGI437	32316902_f2_3	7234	21337	393	131
CONTIGI439	4413392_f3_6	7235	21338	189	63
CONTIGI44	4781505_c2_2	7236	21339	216	72
CONTIGI441	35960061_f1_1	7237	21340	192	64
CONTIGI441	3906252_f3_2	7238	21341	189	63
CONTIGI442	26803752_c1_5	7239	21342	384	128
CONTIGI444	4085925_c1_2	7240	21343	201	67
CONTIGI446	2401038_f2_1	7241	21344	780	260
CONTIGI447	30173462_c2_4	7242	21345	192	64
CONTIGI445	5867837_f3_2	7243	21346	228	76
CONTIGI452	29335950_c3_3	7244	21347	213	71
CONTIGI453	34584805_f1_1	7245	21348	699	233
CONTIGI454	2814013_f2_2	7246	21349	621	207
CONTIGI454	22867812_c2_5	7247	21350	219	73
CONTIGI461	5312535_f2_1	7248	21351	207	69
CONTIGI462	2038912_f2_1	7249	21352	645	215
CONTIGI463	21679052_c1_3	7250	21353	855	285
CONTIGI465	1454566_f2_3	7251	21354	216	72
CONTIGI466	1228427_c1_2	7252	21355	399	133
CONTIGI471	14573755_c3_5	7253	21356	252	84

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CONTIGI510	13678425_f2_1	7287	21390	234	78								
CONTIGI511	24846080_f2_1	7288	21391	582	194								
CONTIGI513	24062512_c3_1	7289	21392	300	100								
CONTIGI518	26645933_f1_1	7290	21393	276	92								
CONTIGI519	10975260_f1_2	7291	21394	201	67								
CONTIGI519	26816927_f3_4	7292	21395	270	90								
CONTIGI520	9812626_f3_1	7293	21396	186	62								
CONTIGI520	24492782_c2_2	7294	21397	195	65								
CONTIGI521	23440875_f1_1	7295	21398	195	65								
CONTIGI521	32289591_f2_3	7296	21399	429	143								
CONTIGI521	26257886_c1_5	7297	21400	1329	443								
CONTIGI523	495787_f1_1	7298	21401	408	136								
CONTIGI525	22065900_f3_2	7299	21402	198	66								
CONTIGI526	36339537_f3_3	7300	21403	288	96								
CONTIGI527	812550_c1_1	7301	21404	249	83								
CONTIGI528	32136265_f2_2	7302	21405	192	64								
CONTIGI528	4406576_c1_4	7303	21406	192	64								
CONTIGI529	33399142_f1_1	7304	21407	204	68								
CONTIGI53	555432_c3_5	7305	21408	489	163								
CONTIGI534	7037782_f2_2	7306	21409	273	91								
CONTIGI535	13958137_f3_3	7307	21410	204	68								
CONTIGI535	980252_f3_4	7308	21411	369	123								
CONTIGI535	2937950_c3_5	7309	21412	198	66								
CONTIGI536	36636588_c3_4	7310	21413	240	80								
CONTIGI537	4977250_f3_4	7311	21414	192	64								
CONTIGI538	4720077_f2_2	7312	21415	297	99								
CONTIGI538	16250393_c3_4	7313	21416	237	79								
CONTIGI539	32595637_f1_1	7314	21417	423	141								
CONTIGI54	11135837_c1_1	7315	21418	192	64								
CONTIGI54	6256312_c1_2	7316	21419	207	69								
CONTIGI540	12923432_f2_1	7317	21420	516	172								
CONTIGI540	1213308_f3_3	7318	21421	198	66								
CONTIGI541	11973151_c2_2	7319	21422	531	177								

CONTIGI542	12923401_c2_6	7320	21423	294	98
CONTIGI544	4101510_c2_3	7321	21424	255	85
CONTIGI545	16454830_f2_3	7322	21425	189	63
CONTIGI545	392050_f3_4	7323	21426	522	174
CONTIGI546	23862763_c1_4	7324	21427	201	67
CONTIGI546	31838286_c2_5	7325	21428	210	70
CONTIGI547	34585765_f1_1	7326	21429	189	63
CONTIGI547	32082526_c1_3	7327	21430	195	65
CONTIGI548	21568786_f2_2	7328	21431	237	79
CONTIGI549	240762_f3_1	7329	21432	345	115
CONTIGI549	23863125_c1_3	7330	21433	231	77
CONTIGI551	19567176_f2_2	7331	21434	276	92
CONTIGI552	24862882_f1_1	7332	21435	270	90
CONTIGI555	23829687_f1_1	7333	21436	537	179
CONTIGI555	31379050_c1_4	7334	21437	204	68
CONTIGI558	24395002_c3_6	7335	21438	267	89
CONTIGI560	5111015_c3_2	7336	21439	189	63
CONTIGI561	36444640_f1_1	7337	21440	348	116
CONTIGI561	21600887_c3_6	7338	21441	249	83
CONTIGI563	970140_c2_3	7339	21442	231	77
CONTIGI566	4865665_c3_5	7340	21443	186	62
CONTIGI567	11976662_f1_1	7341	21444	363	121
CONTIGI567	20314010_f2_2	7342	21445	225	75
CONTIGI567	1365751_c2_4	7343	21446	552	184
CONTIGI569	19613181_c1_1	7344	21447	198	66
CONTIGI57	4111650_f3_2	7345	21448	285	95
CONTIGI57	4064751_c3_3	7346	21449 .	231	77
CONTIGI570	25503431_f2_2	7347	21450	417	139
CONTIGI571	4860961_c3_3	7348	21451	789	263
CONTIGI572	31366305_c1_4	7349	21452	189	63
CONTIGI573	14868752_f2_2	7350	21453	402	134
CONTIGI576	2_c1_7	7351	21454	186	62
CONTIGI578	14665887_c2_3	7352	21455	186	62

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CONTIGI667	553962_c3_6	7419	21522	186	62						
CONTIGI674	392762_c3_2	7420	21523	267	89						
CONTIGI679	2755302_c2_1	7421	21524	261	87						
CONTIGI679	5860637_c3_2	7422	21525	234	78						
CONTIGI68	193811_c1_3	7423	21526	201	67						
CONTIGI68	9923561_c2_4	7424	21527	348	116						
CONTIGI680	6831436_f1_1	7425	21528	222	74						
CONTIGI680	3917562_f1_2	7426	21529	195	65						
CONTIGI680	29488177_c2_4	7427	21530	183	61						
CONTIGI682	31801892_f2_3	7428	21531	207	69						
CONTIGI687	2063800_f3_3	7429	21532	198	66						
CONTIGI687	26773387_c3_6	7430	21533	198	66						
CONTIGI689	12166512_c1_2	7431	21534	243	81						
CONTIGI696	23942152_c1_3	7432	21535	297	99						
CONTIGI697	35351586_c2_3	7433	21536	267	89						
CONTIGI70	22464562_c3_5	7434	21537	201	67						
CONTIGI70	11835142_c3_6	7435	21538	216	72						
CONTIGI700	4742141_c2_2	7436	21539	189	63						
CONTIGI701	4726450_f1_2	7437	21540	660	220						
CONTIGI701	12523392_c1_4	7438	21541	498	166						
CONTIGI702	24786002_f3_3	7439	21542	1053	351						
CONTIGI702	35205382_c3_6	7440	21543	357	119						
CONTIGI703	1409450_c3_4	7441	21544	198	66						
CONTIGI703	13671875_c3_5	7442	21545	354	118						
CONTIGI704	10290807_f3_3	7443	21546	183	61						
CONTIGI704	15912_c3_5	7444	21547	279	93						
CONTIGI707	20345052_f2_1	7445	21548	195	65						
CONTIGI708	22287635_f3_8	7446	21549	249	83						
CONTIGI710	13859437_f3_1	7447	21550	195	65						
CONTIGI711	35440677_f3_1	7448	21551	189	63						
CONTIGI711	24100302_f3_3	7449	21552	801	267						
CONTIGI712	4975682_f2_1	7450	21553	705	235						
CONTIGI714	22767057_c2_2	7451	21554	675	225						

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CONTIG1759	210202_c2_2	7485	21588	201	67							
CONTIG176	19539000_f1_1	7486	21589	189	63							
CONTIG1761	4723313_f1_1	7487	21590	240	80							
CONTIG1763	5939068_c1_2	7488	21591	198	66							
CONTIG1765	24015750_c3_3	7489	21592	186	62							
CONTIG1766	2819525_f2_3	7490	21593	240	80							
CONTIG1767	26377213_f2_1	7491	21594	264	88							
CONTIG1767	3336502_f2_2	7492	21595	372	124							
CONTIG1768	4687531_c1_3	7493	21596	543	181							
CONTIG1769	13165627_c2_2	7494	21597	648	216							
CONTIG1769	860751_c2_3	7495	21598	264	88							
CONTIG1774	26426437_f3_2	7496	21599	1194	398							
CONTIG1775	25579766_f3_1	7497	21600	219	73							
CONTIG1776	14504552_c2_6	7498	21601	315	105							
CONTIG1777	21907276_c3_4	7499	21602	186	62							
CONTIG1780	6681587_f3_3	7500	21603	288	96							
CONTIG1780	30271881_c1_4	7501	21604	264	88							
CONTIG1782	21881451_f1_1	7502	21605	507	169							
CONTIG1782	14657513_f1_2	7503	21606	237	79							
CONTIG1782	23595283_f3_5	7504	21607	261	87							
CONTIG1785	31760052_f1_2	7505	21608	207	69							
CONTIG1786	3946900_f1_1	7506	21609	321	107							
CONTIG1786	2942212_f2_2	7507	21610	633	211							
CONTIG1787	4892186_f3_3	7508	21611	252	84							
CONTIG1789	35166002_f2_1	7509	21612	186	62							
CONTIG1790	20820781_f3_2	7510	21613	873	291							
CONTIG1790	85177_c3_5	7511	21614	195	65							
CONTIG1791	4689378_c2_4	7512	21615	672	224							
CONTIG1792	4687632_c3_4	7513	21616	276	92							
CONTIG1794	22069052_f1_1	7514	21617	210	70							
CONTIG1794	5891333_f1_2	7515	21618	186	62							
CONTIG1794	1210760_c2_3	7516	21619	207	69							
CONTIG1795	25431325_f2_3	7517	21620	207	69							

CONTIGI796	4531437_f1_2	7518	21621	255	85
CONTIGI798	22709505_f2_2	7519	21622	261	87
CONTIGI799	13944051_c1_5	7520	21623	213	71
CONTIGI799	4886380_c3_6	7521	21624	1227	409
CONTIGI80	13100692_c2_5	7522	21625	306	102
CONTIGI800	40037787_c2_1	7523	21626	759	253
CONTIGI802	511457_f2_1	7524	21627	1143	381
CONTIGI805	9897807_f2_4	7525	21628	216	72
CONTIGI805	7114027_c1_5	7526	21629	852	284
CONTIGI808	10632317_f3_1	7527	21630	477	159
CONTIGI808	14943905_c3_3	7528	21631	480	160
CONTIGI81	34179688_c2_3	7529	21632	474	158
CONTIGI810	4353260_f3_5	7530	21633	201	67
CONTIGI810	19766250_c2_7	7531	21634	195	65
CONTIGI810	21650312_c3_9	7532	21635	408	136
CONTIGI812	271952_f3_2	7533	21636	348	116
CONTIGI813	24022762_f3_2	7534	21637	189	63
CONTIGI813	1953175_c1_3	7535	21638	198	66
CONTIGI814	24257786_c2_4	7536	21639	240	80
CONTIGI814	32692188_c3_6	7537	21640	183	61
CONTIGI816	4063915_c2_4	7538	21641	192	64
CONTIGI817	4741377_c1_3	7539	21642	282	94
CONTIGI82	2011457_f2_1	7540	21643	612	204
CONTIGI821	23547502_c2_4	7541	21644	735	245
CONTIGI822	7078427_c2_3	7542	21645	315	105
CONTIGI823	35188317_f1_1	7543	21646	540	180
CONTIGI823	22031706_c1_2	7544	21647	207	69
CONTIGI823	390925_c3_4	7545	21648	255	85
CONTIGI825	15867067_f2_3	7546	21649	999	333
CONTIGI826	43943762_c1_2	7547	21650	798	266
CONTIGI828	25423501_f1_1	7548	21651	426	142
CONTIGI829	2166025_f2_1	7549	21652	921	307
CONTIGI829	29976417_c2_3	7550	21653	210	70

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CONTIG1909	4820441_f3_1	7617	21720	207	69						
CONTIG1910	11885387_c3_5	7618	21721	249	83						
CONTIG1911	10635253_f1_1	7619	21722	1113	371						
CONTIG1912	81882_c2_1	7620	21723	246	82						
CONTIG1914	9806312_f2_4	7621	21724	186	62						
CONTIG1915	792057_c1_1	7622	21725	189	63						
CONTIG1919	4970962_f1_1	7623	21726	267	89						
CONTIG1919	30501892_c2_7	7624	21727	219	73						
CONTIG1920	15714052_f2_1	7625	21728	201	67						
CONTIG1921	36367183_c3_3	7626	21729	363	121						
CONTIG1925	4865950_f1_1	7627	21730	507	169						
CONTIG1925	4344128_f2_4	7628	21731	210	70						
CONTIG1925	12128135_f3_5	7629	21732	597	199						
CONTIG1929	26758388_f1_2	7630	21733	252	84						
CONTIG193	22453138_f1_1	7631	21734	354	118						
CONTIG1931	20428132_c1_4	7632	21735	867	289						
CONTIG1932	10034687_f1_1	7633	21736	204	68						
CONTIG1932	24337752_f3_3	7634	21737	237	79						
CONTIG1935	16523403_f1_2	7635	21738	243	81						
CONTIG1937	10553530_c2_2	7636	21739	1095	365						
CONTIG1938	12634575_f3_3	7637	21740	192	64						
CONTIG1938	100637_c3_6	7638	21741	513	171						
CONTIG1939	4961505_c3_1	7639	21742	321	107						
CONTIG1942	36589213_c1_2	7640	21743	255	85						
CONTIG1942	24241557_c3_3	7641	21744	207	69						
CONTIG1943	12553555_c3_4	7642	21745	240	80						
CONTIG1945	12010417_f1_1	7643	21746	441	147						
CONTIG1945	13868757_f2_2	7644	21747	192	64						
CONTIG1946	4298403_f1_1	7645	21748	237	79						
CONTIG1946	9797753_f2_3	7646	21749	249	83						
CONTIG1949	24614137_f3_1	7647	21750	201	67						
CONTIG1953	6038128_c2_6	7648	21751	723	241						
CONTIG1954	1464430_f2_3	7649	21752	531	177						

CONTIG1954	35346942_c1_7	7650	21753	207	69						
CONTIG1955	22445326_f1_1	7651	21754	405	135						
CONTIG1955	2929511_f2_5	7652	21755	312	104						
CONTIG1959	4141005_c1_3	7653	21756	210	70						
CONTIG196	23651410_f1_1	7654	21757	558	186						
CONTIG196	25601066_c2_4	7655	21758	306	102						
CONTIG1960	4694055_c2_7	7656	21759	441	147						
CONTIG1963	82502_f1_1	7657	21760	1479	493						
CONTIG1964	35196913_c1_2	7658	21761	285	95						
CONTIG1966	23925400_f2_2	7659	21762	912	304						
CONTIG1966	11719216_f3_3	7660	21763	390	130						
CONTIG1968	19562586_c1_3	7661	21764	417	139						
CONTIG1970	23600887_c1_2	7662	21765	225	75						
CONTIG1970	32627_c2_4	7663	21766	192	64						
CONTIG1971	34567840_c2_6	7664	21767	1089	363						
CONTIG1972	16220432_c1_4	7665	21768	585	195						
CONTIG1973	22275425_f3_1	7666	21769	219	73						
CONTIG1973	19628812_c2_3	7667	21770	183	61						
CONTIG1974	34614062_c3_7	7668	21771	294	98						
CONTIG1975	29801500_f2_2	7669	21772	204	68						
CONTIG1982	26438_c2_4	7670	21773	189	63						
CONTIG1983	30517700_c1_2	7671	21774	195	65						
CONTIG1983	35423410_c1_3	7672	21775	300	100						
CONTIG1985	21692875_f1_1	7673	21776	222	74						
CONTIG1986	10632757_f1_1	7674	21777	972	324						
CONTIG1986	26772175_c3_3	7675	21778	228	76						
CONTIG1987	12115943_c1_5	7676	21779	408	136						
CONTIG1990	5353467_f3_3	7677	21780	498	166						
CONTIG1991	14494061_f2_2	7678	21781	627	209						
CONTIG1992	21696938_f1_2	7679	21782	186	62						
CONTIG1994	4328311_c1_4	7680	21783	231	77						
CONTIG1994	12582927_c2_5	7681	21784	564	188						
CONTIG1995	973535_c2_2	7682	21785	246	82						







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CONTIG2188	21496056_c3_2	7848	21951	216	72
CONTIG2194	25675936_f3_3	7849	21952	483	161
CONTIG2195	1953175_f2_1	7850	21953	198	66
CONTIG2195	24022762_c1_4	7851	21954	198	66
CONTIG2196	2039582_c1_2	7852	21955	258	86
CONTIG2199	11879628_f1_2	7853	21956	207	69
CONTIG2199	29875627_f3_6	7854	21957	225	75
CONTIG2199	4765887_c1_7	7855	21958	300	100
CONTIG2200	33707062_c1_3	7856	21959	879	293
CONTIG2201	17596083_c3_2	7857	21960	240	80
CONTIG2202	24019382_f1_1	7858	21961	1119	373
CONTIG2204	35429578_c2_9	7859	21962	408	136
CONTIG2208	15633583_f3_4	7860	21963	216	72
CONTIG221	786550_c3_2	7861	21964	396	132
CONTIG2211	6829787_f1_1	7862	21965	243	81
CONTIG2211	890941_c1_6	7863	21966	192	64
CONTIG2214	15630250_c1_4	7864	21967	192	64
CONTIG2215	1052151_c3_7	7865	21968	261	87
CONTIG2216	12287803_f3_2	7866	21969	198	66
CONTIG222	7812_c1_1	7867	21970	186	62
CONTIG222	24297127_c2_2	7868	21971	216	72
CONTIG2220	4803911_c1_2	7869	21972	183	61
CONTIG2222	22454663_f1_1	7870	21973	210	70
CONTIG2222	9957807_f2_3	7871	21974	408	136
CONTIG2223	1223838_f3_2	7872	21975	201	67
CONTIG2225	14159376_c3_4	7873	21976	183	61
CONTIG2226	26697131_f1_1	7874	21977	1251	417
CONTIG2228	26297137_f2_1	7875	21978	228	76
CONTIG223	26836712_f1_1	7876	21979	246	82
CONTIG223	35976557_f2_2	7877	21980	198	66
CONTIG2233	10159531_f2_1	7878	21981	1095	365
CONTIG2234	4860307_c3_9	7879	21982	582	194
CONTIG2236	4975827_c3_2	7880	21983	276	92

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CONTIG2350	4820450_f2_1	7980	22083	663	221								
CONTIG2351	8225067_f2_2	7981	22084	237	79								
CONTIG2352	29453377_c3_4	7982	22085	357	119								
CONTIG2353	33864625_f2_2	7983	22086	270	90								
CONTIG2354	21640903_f1_1	7984	22087	456	152								
CONTIG2354	1441543_c3_6	7985	22088	432	144								
CONTIG2357	15626632_f2_2	7986	22089	255	85								
CONTIG2358	4562512_c1_3	7987	22090	570	190								
CONTIG2359	22442202_f1_2	7988	22091	288	96								
CONTIG2360	4315875_f2_3	7989	22092	597	199								
CONTIG2362	27234751_f1_1	7990	22093	276	92								
CONTIG2365	7221010_c1_3	7991	22094	318	106								
CONTIG2367	20329055_c2_2	7992	22095	606	202								
CONTIG2368	26370338_f2_4	7993	22096	216	72								
CONTIG2368	26382952_c3_5	7994	22097	495	165								
CONTIG237	23910382_c2_2	7995	22098	189	63								
CONTIG2371	6098437_c2_4	7996	22099	306	102								
CONTIG2373	12993780_f3_1	7997	22100	849	283								
CONTIG2374	196875_f3_2	7998	22101	204	68								
CONTIG2375	34495328_c3_4	7999	22102	273	91								
CONTIG2375	6931552_c3_5	8000	22103	498	166								
CONTIG2378	10657587_f2_1	8001	22104	393	131								
CONTIG2381	9844058_f2_2	8002	22105	243	81								
CONTIG2381	1960888_f3_4	8003	22106	198	66								
CONTIG2381	1367142_c1_5	8004	22107	198	66								
CONTIG2382	36292_f1_2	8005	22108	231	77								
CONTIG2382	21985877_f3_4	8006	22109	369	123								
CONTIG2385	6641092_f1_1	8007	22110	189	63								
CONTIG2385	36306_f3_2	8008	22111	234	78								
CONTIG2386	26384555_f2_1	8009	22112	234	78								
CONTIG2387	24648436_f2_2	8010	22113	492	164								
CONTIG2387	23835912_f2_3	8011	22114	234	78								
CONTIG2387	10650288_c3_5	8012	22115	825	275								



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CONTIG2576	26594050_f1_2	8178	22281	225	75
CONTIG2576	4298162_c2_3	8179	22282	330	110
CONTIG2577	5948961_f1_1	8180	22283	264	88
CONTIG2577	4307182_c1_2	8181	22284	483	161
CONTIG2578	24495442_c3_6	8182	22285	186	62
CONTIG2579	15668_f3_2	8183	22286	291	97
CONTIG2579	12587805_f3_4	8184	22287	249	83
CONTIG2579	19548501_c3_6	8185	22288	195	65
CONTIG2580	10011687_f3_4	8186	22289	279	93
CONTIG2581	1445137_c2_6	8187	22290	852	284
CONTIG2583	24609786_c1_3	8188	22291	264	88
CONTIG2584	22750637_f1_1	8189	22292	399	133
CONTIG2584	32537502_f3_3	8190	22293	195	65
CONTIG2584	961567_f3_4	8191	22294	342	114
CONTIG2584	24392180_c1_6	8192	22295	240	80
CONTIG2588	14585392_f3_2	8193	22296	192	64
CONTIG2591	6834637_c2_2	8194	22297	942	314
CONTIG2592	4957842_f2_4	8195	22298	186	62
CONTIG2592	12312910_c2_9	8196	22299	249	83
CONTIG2592	13756450_c3_10	8197	22300	471	157
CONTIG2593	5364012_f2_1	8198	22301	240	80
CONTIG2593	4190932_c2_3	8199	22302	201	67
CONTIG2595	20319406_f1_1	8200	22303	210	70
CONTIG2595	4938275_c1_3	8201	22304	183	61
CONTIG2596	22004425_f1_1	8202	22305	1140	380
CONTIG2597	14506905_f3_4	8203	22306	276	92
CONTIG2597	6645252_c3_5	8204	22307	294	98
CONTIG26	25585899_c1_2	8205	22308	279	93
CONTIG2601	21515925_f1_1	8206	22309	495	165
CONTIG2603	24413937_f1_1	8207	22310	219	73
CONTIG2605	12696057_f1_1	8208	22311	246	82
CONTIG2605	26502_f1_2	8209	22312	834	278
CONTIG2607	262_c1_4	8210	22313	198	66



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CONTIG2754	6125402_c2_3	8343	22446	186	62							
CONTIG2756	25582056_f2_1	8344	22447	201	67							
CONTIG2756	36601503_c3_4	8345	22448	270	90							
CONTIG2757	23868800_c1_4	8346	22449	741	247							
CONTIG2758	4063377_f2_1	8347	22450	504	168							
CONTIG2761	10058137_c3_3	8348	22451	219	73							
CONTIG2762	1220056_c1_3	8349	22452	264	88							
CONTIG2764	22160028_f2_5	8350	22453	375	125							
CONTIG2764	12381718_c1_9	8351	22454	183	61							
CONTIG2765	14652300_f3_1	8352	22455	213	71							
CONTIG2766	33210752_f3_3	8353	22456	354	118							
CONTIG2766	392275_c1_4	8354	22457	282	94							
CONTIG2768	29489550_c1_2	8355	22458	213	71							
CONTIG2768	4023577_c1_3	8356	22459	183	61							
CONTIG2769	189001_c3_4	8357	22460	264	88							
CONTIG2770	13867211_c2_1	8358	22461	261	87							
CONTIG2770	4197917_c3_3	8359	22462	222	74							
CONTIG2771	24617250_c1_4	8360	22463	183	61							
CONTIG2771	22707561_c2_5	8361	22464	717	239							
CONTIG2772	35798263_f3_2	8362	22465	405	135							
CONTIG2772	782818_c1_4	8363	22466	201	67							
CONTIG2773	2166340_f2_2	8364	22467	501	167							
CONTIG2773	971968_c2_3	8365	22468	939	313							
CONTIG2775	2478180_c1_3	8366	22469	243	81							
CONTIG2776	24219206_f1_3	8367	22470	213	71							
CONTIG2778	4882205_f2_2	8368	22471	363	121							
CONTIG2778	6850425_f3_4	8369	22472	258	86							
CONTIG278	34412805_f2_1	8370	22473	207	69							
CONTIG2786	13864555_f3_1	8371	22474	687	229							
CONTIG2787	24399093_f2_2	8372	22475	204	68							
CONTIG2788	1992262_f2_2	8373	22476	237	79							
CONTIG2788	4533402_c1_5	8374	22477	270	90							
CONTIG2789	24226675_f1_1	8375	22478	252	84							

CONTIG2790	14489681_f2_2	8376	22479	291	97								
CONTIG2790	33469056_c2_5	8377	22480	282	94								
CONTIG2792	24492252_f3_4	8378	22481	612	204								
CONTIG2792	24424055_c3_6	8379	22482	303	101								
CONTIG2793	25563888_f2_2	8380	22483	192	64								
CONTIG2793	10626530_f2_4	8381	22484	639	213								
CONTIG2796	5975336_f3_3	8382	22485	219	73								
CONTIG2796	21552817_c2_6	8383	22486	246	82								
CONTIG2799	2813177_c3_5	8384	22487	753	251								
CONTIG2801	24876955_c2_12	8385	22488	540	180								
CONTIG2803	35736627_f3_2	8386	22489	330	110								
CONTIG2803	26448562_f3_3	8387	22490	198	66								
CONTIG2803	11725001_c2_6	8388	22491	192	64								
CONTIG2807	5126450_f1_1	8389	22492	291	97								
CONTIG2807	24786265_f3_2	8390	22493	183	61								
CONTIG2810	29772135_c1_2	8391	22494	186	62								
CONTIG2813	1173763_f2_3	8392	22495	213	71								
CONTIG2814	9797505_f1_1	8393	22496	333	111								
CONTIG2816	2343801_c1_7	8394	22497	201	67								
CONTIG2817	24892187_f2_1	8395	22498	1713	571								
CONTIG2818	24429561_f2_1	8396	22499	1743	581								
CONTIG2819	23851415_f1_1	8397	22500	198	66								
CONTIG282	2164763_c2_2	8398	22501	486	162								
CONTIG2820	10831531_f3_2	8399	22502	282	94								
CONTIG2820	24253878_c1_5	8400	22503	222	74								
CONTIG2821	24023411_c2_3	8401	22504	1632	544								
CONTIG2823	24257887_f1_2	8402	22505	186	62								
CONTIG2825	24023262_c1_1	8403	22506	219	73								
CONTIG2828	15783540_f1_1	8404	22507	189	63								
CONTIG2829	2131260_f2_3	8405	22508	279	93								
CONTIG2830	869802_c3_5	8406	22509	183	61								
CONTIG2832	10057318_f1_1	8407	22510	834	278								
CONTIG2832	4890638_c1_2	8408	22511	285	95								

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CONTIG309	21679640_c3_2	8674	22777	216	72
CONTIG3090	1298316_f1_1	8675	22778	780	260
CONTIG3092	1198276_f1_1	8676	22779	204	68
CONTIG3092	12691937_c1_4	8677	22780	207	69
CONTIG3092	23913888_c2_6	8678	22781	255	85
CONTIG3093	20709712_f1_2	8679	22782	255	85
CONTIG3094	24413312_f1_1	8680	22783	186	62
CONTIG3094	22832952_f1_2	8681	22784	1008	336
CONTIG3094	3165813_f2_5	8682	22785	399	133
CONTIG3095	433332_f3_3	8683	22786	1032	344
CONTIG3097	13679590_c3_4	8684	22787	237	79
CONTIG3098	25397150_f3_2	8685	22788	234	78
CONTIG3099	23600427_f3_5	8686	22789	528	176
CONTIG3099	22363281_c2_6	8687	22790	240	80
CONTIG310	11173430_f3_1	8688	22791	231	77
CONTIG3102	4535066_c2_2	8689	22792	222	74
CONTIG3104	4460881_f1_2	8690	22793	186	62
CONTIG3104	1074012_f3_5	8691	22794	426	142
CONTIG3105	4097008_f3_6	8692	22795	324	108
CONTIG3106	26290938_f1_2	8693	22796	195	65
CONTIG3106	29688750_c1_9	8694	22797	369	123
CONTIG3108	12694102_f1_1	8695	22798	489	163
CONTIG3108	4535066_f1_2	8696	22799	243	81
CONTIG3108	9769002_f1_3	8697	22800	213	71
CONTIG3108	6642006_f3_4	8698	22801	201	67
CONTIG3109	24019686_f3_2	8699	22802	465	155
CONTIG3109	10831387_c3_5	8700	22803	474	158
CONTIG311	20507192_c1_2	8701	22804	189	63
CONTIG3110	34163962_f2_3	8702	22805	477	159
CONTIG3110	156250_f3_6	8703	22806	213	71
CONTIG3111	21914206_f1_1	8704	22807	186	62
CONTIG3112	4955080_c3_5	8705	22808	591	197

CONTIG3113	13789032_f3_2	8706	22809	891	297
CONTIG3115	957502_f2_1	8707	22810	201	67
CONTIG3116	15784441_f3_3	8708	22811	384	128
CONTIG3117	16797136_c3_8	8709	22812	603	201
CONTIG3118	33714388_c2_2	8710	22813	201	67
CONTIG3120	25423202_c3_2	8711	22814	576	192
CONTIG3121	3939385_f1_1	8712	22815	321	107
CONTIG3121	9788937_f3_9	8713	22816	300	100
CONTIG3121	24426692_f3_10	8714	22817	279	93
CONTIG3121	4801436_f3_11	8715	22818	858	286
CONTIG3121	4957928_c3_13	8716	22819	285	95
CONTIG3123	2166652_f1_1	8717	22820	543	181
CONTIG3123	24431642_f2_2	8718	22821	210	70
CONTIG3123	7047512_c3_5	8719	22822	213	71
CONTIG3124	1260062_c2_5	8720	22823	1461	487
CONTIG3125	36040788_f3_3	8721	22824	312	104
CONTIG3125	19542550_c3_9	8722	22825	183	61
CONTIG3126	10976527_f1_1	8723	22826	636	212
CONTIG3127	6741260_f3_1	8724	22827	225	75
CONTIG3128	10000313_c3_3	8725	22828	576	192
CONTIG3130	22657162_f2_2	8726	22829	195	65
CONTIG3130	547010_c1_3	8727	22830	198	66
CONTIG3130	24220001_c3_6	8728	22831	324	108
CONTIG3131	2915892_f2_2	8729	22832	219	73
CONTIG3131	31901952_c3_3	8730	22833	192	64
CONTIG3134	2345281_f2_2	8731	22834	1068	356
CONTIG3134	24650130_f3_3	8732	22835	264	88
CONTIG3134	24332176_c1_5	8733	22836	195	65
CONTIG3137	16253840_c3_6	8734	22837	1320	440
CONTIG3138	26600777_f2_1	8735	22838	186	62
CONTIG3139	12516512_f3_3	8736	22839	204	68
CONTIG314	35422253_f2_1	8737	22840	234	78
CONTIG314	15709636_f2_2	8738	22841	222	74



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CONTIG3199	34406700_f1_1	8805	22908	186	62
CONTIG3199	2820377_f1_2	8806	22909	234	78
CONTIG3199	25942308_c2_8	8807	22910	693	231
CONTIG32	22948767_f1_1	8808	22911	270	90
CONTIG3200	3990763_f2_3	8809	22912	327	109
CONTIG3201	10751967_f2_1	8810	22913	363	121
CONTIG3201	26376078_c3_9	8811	22914	438	146
CONTIG3202	23397187_f3_1	8812	22915	225	75
CONTIG3203	14223750_c1_2	8813	22916	1152	384
CONTIG3203	34179756_c3_3	8814	22917	210	70
CONTIG3204	33461626_c3_5	8815	22918	204	68
CONTIG3209	29488537_f3_2	8816	22919	213	71
CONTIG3211	4297215_c1_7	8817	22920	1485	495
CONTIG3212	24789037_f3_3	8818	22921	285	95
CONTIG3213	16053375_c1_2	8819	22922	252	84
CONTIG3218	6647762_c1_5	8820	22923	222	74
CONTIG3218	26755280_c1_7	8821	22924	435	145
CONTIG3218	36448452_c2_8	8822	22925	201	67
CONTIG3219	23395662_f1_1	8823	22926	201	67
CONTIG3219	10031510_c3_8	8824	22927	585	195
CONTIG322	14564567_f2_1	8825	22928	714	238
CONTIG3220	24015680_c2_4	8826	22929	231	77
CONTIG3222	26822293_f3_7	8827	22930	201	67
CONTIG3222	34198462_c3_11	8828	22931	354	118
CONTIG3225	5993802_f3_2	8829	22932	240	80
CONTIG3227	10190906_c1_3	8830	22933	240	80
CONTIG3227	23603463_c2_7	8831	22934	225	75
CONTIG3228	1441332_f1_1	8832	22935	288	96
CONTIG3228	3956537_f1_2	8833	22936	267	89
CONTIG3229	31295207_c3_7	8834	22937	207	69
CONTIG3230	25423885_f1_1	8835	22938	312	104
CONTIG3230	157500_f1_2	8836	22939	525	175
CONTIG3230	4692152_f2_3	8837	22940	237	79

CONTIG3230	594175_f3_4	8838	22941	246	82
CONTIG3230	29533140_c3_6	8839	22942	324	108
CONTIG3231	22657635_f1_1	8840	22943	720	240
CONTIG3235	25556255_c3_4	8841	22944	189	63
CONTIG3235	30707575_c3_5	8842	22945	183	61
CONTIG3237	21618957_f1_1	8843	22946	309	103
CONTIG3238	24490927_f2_2	8844	22947	225	75
CONTIG3238	16209750_f3_3	8845	22948	189	63
CONTIG3239	34664018_f2_3	8846	22949	186	62
CONTIG3240	34033450_f2_2	8847	22950	201	67
CONTIG3240	34572068_f2_3	8848	22951	201	67
CONTIG3240	34064378_f3_4	8849	22952	261	87
CONTIG3240	6645012_c2_6	8850	22953	204	68
CONTIG3240	2132807_c3_7	8851	22954	492	164
CONTIG3242	9944505_f3_2	8852	22955	648	216
CONTIG3243	6048402_c2_3	8853	22956	279	93
CONTIG3244	22308161_f1_1	8854	22957	567	189
CONTIG3246	20444002_f3_1	8855	22958	210	70
CONTIG3247	25938966_f3_1	8856	22959	354	118
CONTIG3247	14586580_f3_2	8857	22960	309	103
CONTIG3248	4818878_c2_6	8858	22961	669	223
CONTIG3249	24804681_f2_2	8859	22962	219	73
CONTIG325	24098875_f3_2	8860	22963	519	173
CONTIG3250	1456275_f1_1	8861	22964	204	68
CONTIG3250	33994057_c1_3	8862	22965	378	126
CONTIG3250	4192163_c2_5	8863	22966	264	88
CONTIG3251	24070342_f2_2	8864	22967	183	61
CONTIG3252	20489501_c1_5	8865	22968	201	67
CONTIG3253	26366262_c3_6	8866	22969	231	77
CONTIG3254	393760_f1_1	8867	22970	201	67
CONTIG3255	13867937_c2_4	8868	22971	744	248
CONTIG3256	1204643_f3_3	8869	22972	216	72
CONTIG3259	24324062_c2_6	8870	22973	717	239



CONTIG3286	19689125_f1_3	8904	23007	396	132
CONTIG3286	4532817_f3_4	8905	23008	228	76
CONTIG3288	822135_c1_1	8906	23009	1107	369
CONTIG3288	819436_c3_3	8907	23010	210	70
CONTIG3290	6835887_c3_3	8908	23011	1176	392
CONTIG3291	4116658_f2_2	8909	23012	339	113
CONTIG3293	1346910_f2_1	8910	23013	1680	560
CONTIG3294	9885830_f3_2	8911	23014	279	93
CONTIG3296	391925_c2_7	8912	23015	189	63
CONTIG3297	24801063_c1_7	8913	23016	279	93
CONTIG3298	1409657_c2_2	8914	23017	879	293
CONTIG3299	30089638_f3_3	8915	23018	183	61
CONTIG3300	4771937_c1_6	8916	23019	240	80
CONTIG3301	4142508_c3_3	8917	23020	861	287
CONTIG3303	22900762_f1_1	8918	23021	201	67
CONTIG3305	5972127_f2_3	8919	23022	228	76
CONTIG3305	35429578_f3_4	8920	23023	354	118
CONTIG3305	4711657_c3_10	8921	23024	210	70
CONTIG3306	3306375_c1_3	8922	23025	213	71
CONTIG3307	25423561_c1_4	8923	23026	2064	688
CONTIG3309	23494793_f2_1	8924	23027	228	76
CONTIG331	16970461_c3_1	8925	23028	585	195
CONTIG3310	35156540_c2_6	8926	23029	357	119
CONTIG3311	29688750_f3_6	8927	23030	369	123
CONTIG3313	58557_c1_8	8928	23031	216	72
CONTIG3314	960336_f1_1	8929	23032	201	67
CONTIG3314	26365927_c1_6	8930	23033	234	78
CONTIG3314	4189077_c2_10	8931	23034	1188	396
CONTIG3316	30556530_c1_2	8932	23035	702	234
CONTIG3317	36111013_f1_1	8933	23036	201	67
CONTIG3317	33859576_f3_5	8934	23037	267	89
CONTIG3318	792137_f3_4	8935	23038	387	129
CONTIG3319	6735133_f2_1	8936	23039	1386	462

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CONTIG3419	33252018_f2_3	9069	23172	189	63						
CONTIG3419	4303531_f2_4	9070	23173	339	113						
CONTIG3420	35255176_c1_3	9071	23174	186	62						
CONTIG3422	23479566_f3_2	9072	23175	264	88						
CONTIG3423	29736250_f1_1	9073	23176	222	74						
CONTIG3423	5270436_c1_6	9074	23177	189	63						
CONTIG3423	33395312_c3_8	9075	23178	216	72						
CONTIG3424	24491061_c2_4	9076	23179	192	64						
CONTIG343	13750317_f1_1	9077	23180	495	165						
CONTIG343	4176678_c2_4	9078	23181	285	95						
CONTIG3431	54775_c1_2	9079	23182	1170	390						
CONTIG3431	4100817_c3_4	9080	23183	198	66						
CONTIG3431	898261_c3_5	9081	23184	255	85						
CONTIG3432	24414056_c1_10	9082	23185	204	68						
CONTIG3433	2913930_f2_1	9083	23186	219	73						
CONTIG3435	25469653_c3_2	9084	23187	1671	557						
CONTIG3436	35162837_c1_5	9085	23188	192	64						
CONTIG3436	34022717_c1_6	9086	23189	279	93						
CONTIG3438	7057025_f2_1	9087	23190	561	187						
CONTIG344	10196957_f3_1	9088	23191	321	107						
CONTIG3440	14742187_c3_10	9089	23192	732	244						
CONTIG3442	19533312_c1_4	9090	23193	183	61						
CONTIG3442	19937876_c3_5	9091	23194	489	163						
CONTIG3443	14878436_c3_4	9092	23195	309	103						
CONTIG3444	12212777_f1_2	9093	23196	228	76						
CONTIG3444	6050717_f3_5	9094	23197	942	314						
CONTIG3445	10828550_f3_2	9095	23198	282	94						
CONTIG3447	25993837_f1_1	9096	23199	336	112						
CONTIG3447	3132692_f2_2	9097	23200	2100	700						
CONTIG3447	6814078_f3_7	9098	23201	726	242						
CONTIG3449	34464410_c3_1	9099	23202	333	111						
CONTIG3450	24507276_c1_3	9100	23203	891	297						
CONTIG3452	1446050_c1_5	9101	23204	621	207						

CONTIG3454	32537662_f1_1	9102	23205	195	65						
CONTIG3454	4882811_f2_3	9103	23206	255	85						
CONTIG3454	19734441_c1_5	9104	23207	195	65						
CONTIG3455	22664567_c2_5	9105	23208	1326	442						
CONTIG3457	4095313_f2_5	9106	23209	528	176						
CONTIG3457	14063912_c1_11	9107	23210	780	260						
CONTIG3458	21881592_c1_8	9108	23211	585	195						
CONTIG3461	22946885_f1_1	9109	23212	192	64						
CONTIG3461	970327_c3_13	9110	23213	504	168						
CONTIG3464	32664032_f2_2	9111	23214	189	63						
CONTIG3464	23469050_f3_3	9112	23215	222	74						
CONTIG3464	10978462_c2_7	9113	23216	756	252						
CONTIG3466	29454825_c2_2	9114	23217	231	77						
CONTIG3467	34385313_f3_1	9115	23218	219	73						
CONTIG3467	1381257_c3_4	9116	23219	237	79						
CONTIG3468	444135_c2_7	9117	23220	186	62						
CONTIG3468	9800817_c3_8	9118	23221	195	65						
CONTIG3469	21687825_f3_3	9119	23222	198	66						
CONTIG3470	4895010_c2_6	9120	23223	330	110						
CONTIG3471	22554712_f3_3	9121	23224	201	67						
CONTIG3473	16595900_c2_4	9122	23225	903	301						
CONTIG3476	398502_f1_2	9123	23226	249	83						
CONTIG3476	4312510_f2_3	9124	23227	201	67						
CONTIG3476	25425651_f2_5	9125	23228	891	297						
CONTIG3476	16039665_c3_7	9126	23229	186	62						
CONTIG3477	5941937_f1_1	9127	23230	186	62						
CONTIG3479	4298302_c2_9	9128	23231	225	75						
CONTIG348	21675277_f3_3	9129	23232	258	86						
CONTIG3481	33398535_f2_3	9130	23233	234	78						
CONTIG3481	5194640_c1_4	9131	23234	600	200						
CONTIG3481	9843750_c3_6	9132	23235	669	223						
CONTIG3483	10970305_f2_2	9133	23236	1149	383						
CONTIG3484	16446961_f1_1	9134	23237	204	68						

CONTIG3484	4882826_f1_2	9135	23238	186	62
CONTIG3484	4901577_f2_4	9136	23239	195	65
CONTIG3484	23953550_c1_5	9137	23240	201	67
CONTIG3484	26564212_c3_8	9138	23241	201	67
CONTIG3485	3322163_c2_3	9139	23242	894	298
CONTIG3487	400075_f2_2	9140	23243	213	71
CONTIG3487	31453450_f3_3	9141	23244	240	80
CONTIG3488	3989050_f2_2	9142	23245	183	61
CONTIG3488	1964127_c3_5	9143	23246	219	73
CONTIG3489	23928375_f3_3	9144	23247	231	77
CONTIG3490	567311_f1_2	9145	23248	309	103
CONTIG3492	12110777_f1_1	9146	23249	237	79
CONTIG3492	24709461_f3_5	9147	23250	396	132
CONTIG3492	1353153_c2_6	9148	23251	210	70
CONTIG3493	5861062_f2_1	9149	23252	288	96
CONTIG3493	14625252_c3_6	9150	23253	207	69
CONTIG3494	23454702_f1_3	9151	23254	213	71
CONTIG3494	29507800_f2_4	9152	23255	1167	389
CONTIG3494	29879715_f2_5	9153	23256	264	88
CONTIG3495	13941876_f1_2	9154	23257	660	220
CONTIG3495	5319205_f2_3	9155	23258	243	81
CONTIG3495	16677042_c2_6	9156	23259	186	62
CONTIG3496	5985880_c3_6	9157	23260	198	66
CONTIG3497	24901562_f3_4	9158	23261	189	63
CONTIG3497	9939775_f3_5	9159	23262	231	77
CONTIG3498	6831590_c2_10	9160	23263	720	240
CONTIG350	14735908_f3_1	9161	23264	219	73
CONTIG3500	42192_c1_9	9162	23265	219	73
CONTIG3500	25679637_c1_10	9163	23266	264	88
CONTIG3500	5080392_c3_15	9164	23267	192	64
CONTIG3501	1260_c2_4	9165	23268	216	72
CONTIG3501	26751507_c3_5	9166	23269	267	89
CONTIG3502	16179038_f1_1	9167	23270	534	178





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CONTIG3677	10558467_c3_7	9366	23469	249	83
CONTIG3678	6054038_f1_1	9367	23470	288	96
CONTIG3678	822338_f1_2	9368	23471	201	67
CONTIG3678	23444677_c2_5	9369	23472	201	67
CONTIG3681	14079686_f1_1	9370	23473	249	83
CONTIG3682	209717_c3_10	9371	23474	186	62
CONTIG3683	24017026_f3_2	9372	23475	219	73
CONTIG3685	22925127_f3_3	9373	23476	186	62
CONTIG3685	25500312_c2_4	9374	23477	183	61
CONTIG3686	22031575_f1_1	9375	23478	906	302
CONTIG3688	23941502_f3_2	9376	23479	633	211
CONTIG3689	4421937_f3_3	9377	23480	330	110
CONTIG3691	35807755_f2_1	9378	23481	444	148
CONTIG3691	234576_f3_3	9379	23482	354	118
CONTIG3691	9850437_c1_4	9380	23483	1263	421
CONTIG3692	79653_c2_6	9381	23484	615	205
CONTIG3693	24313893_c1_3	9382	23485	279	93
CONTIG3694	34008436_f2_2	9383	23486	237	79
CONTIG3694	16839700_c3_8	9384	23487	834	278
CONTIG3695	10594392_f2_4	9385	23488	222	74
CONTIG3695	35354827_c2_7	9386	23489	738	246
CONTIG3697	26562530_f2_3	9387	23490	189	63
CONTIG3698	24064632_f3_4	9388	23491	261	87
CONTIG3701	93_c2_6	9389	23492	183	61
CONTIG3704	24470063_c2_4	9390	23493	561	187
CONTIG3705	5094636_f1_1	9391	23494	681	227
CONTIG3705	14879378_f2_3	9392	23495	195	65
CONTIG3708	23444752_c1_6	9393	23496	186	62
CONTIG3709	34174031_f2_3	9394	23497	213	71
CONTIG3710	19665683_c2_8	9395	23498	1194	398
CONTIG3710	14720327_c2_9	9396	23499	186	62
CONTIG3712	87561_c2_6	9397	23500	195	65
CONTIG3712	4328937_c2_7	9398	23501	738	246

CONTIG3714	9959385_f1_1	9399	23502	201	67						
CONTIG3714	23988762_c2_4	9400	23503	255	85						
CONTIG3714	16926001_c3_5	9401	23504	207	69						
CONTIG3715	20082160_c3_7	9402	23505	240	80						
CONTIG3716	259386_c3_9	9403	23506	390	130						
CONTIG3717	5078200_c1_5	9404	23507	243	81						
CONTIG3717	34381502_c1_7	9405	23508	297	99						
CONTIG3718	4687575_f3_5	9406	23509	243	81						
CONTIG3718	10660933_c1_7	9407	23510	327	109						
CONTIG3720	22445177_c1_4	9408	23511	393	131						
CONTIG3720	10819003_c1_5	9409	23512	282	94						
CONTIG3720	24339051_c2_6	9410	23513	612	204						
CONTIG3721	24414012_f1_1	9411	23514	279	93						
CONTIG3723	5972252_f3_4	9412	23515	195	65						
CONTIG3727	4821942_f2_3	9413	23516	318	106						
CONTIG3727	176892_f3_5	9414	23517	189	63						
CONTIG3728	34579626_f2_2	9415	23518	198	66						
CONTIG3728	20390926_c1_5	9416	23519	249	83						
CONTIG3728	22078552_c2_7	9417	23520	201	67						
CONTIG3728	19953140_c3_10	9418	23521	285	95						
CONTIG3729	24093840_f2_3	9419	23522	213	71						
CONTIG3730	2910812_f1_1	9420	23523	216	72						
CONTIG3730	13680192_f1_2	9421	23524	225	75						
CONTIG3730	1972127_f3_7	9422	23525	183	61						
CONTIG3730	36532887_c1_9	9423	23526	213	71						
CONTIG3730	21928137_c2_10	9424	23527	207	69						
CONTIG3731	9843930_f2_8	9425	23528	210	70						
CONTIG3731	2110306_c2_15	9426	23529	444	148						
CONTIG3732	23844008_f1_3	9427	23530	309	103						
CONTIG3732	11723200_c1_4	9428	23531	207	69						
CONTIG3735	2770337_f2_6	9429	23532	543	181						
CONTIG3735	20350808_c1_11	9430	23533	189	63						
CONTIG3737	11225691_f2_1	9431	23534	279	93						



CONTIG3760	14063150_c3_6	9465	23568	267	89
CONTIG3761	6097512_f2_2	9466	23569	222	74
CONTIG3761	35156256_f3_3	9467	23570	216	72
CONTIG3761	3017817_c2_9	9468	23571	222	74
CONTIG3761	12539000_c3_11	9469	23572	186	62
CONTIG3764	881910_f3_3	9470	23573	261	87
CONTIG3764	33369142_c1_5	9471	23574	246	82
CONTIG3765	14095443_f1_1	9472	23575	240	80
CONTIG3770	24615680_c3_5	9473	23576	204	68
CONTIG3771	22070202_f3_6	9474	23577	204	68
CONTIG3773	178_f1_1	9475	23578	189	63
CONTIG3773	12912588_f3_5	9476	23579	228	76
CONTIG3773	6664050_c1_6	9477	23580	243	81
CONTIG3774	24647250_f1_1	9478	23581	195	65
CONTIG3774	14455175_c3_6	9479	23582	216	72
CONTIG3777	23990877_f1_1	9480	23583	189	63
CONTIG3777	13962833_c2_5	9481	23584	1155	385
CONTIG3779	14176537_c2_8	9482	23585	246	82
CONTIG378	986038_f2_1	9483	23586	294	98
CONTIG3780	4306537_c2_5	9484	23587	531	177
CONTIG3782	235700_c1_4	9485	23588	732	244
CONTIG3783	2548377_c3_9	9486	23589	243	81
CONTIG3785	10838882_f1_1	9487	23590	711	237
CONTIG3787	23444382_f1_1	9488	23591	306	102
CONTIG3789	882937_f2_2	9489	23592	342	114
CONTIG3790	33782837_f2_2	9490	23593	261	87
CONTIG3791	30275337_f3_3	9491	23594	294	98
CONTIG3792	23828302_f1_1	9492	23595	450	150
CONTIG3792	29501590_f2_6	9493	23596	195	65
CONTIG3793	32428956_f3_2	9494	23597	1386	462
CONTIG3795	22065900_c1_4	9495	23598	195	65
CONTIG3796	11812626_f1_1	9496	23599	720	240
CONTIG3797	9770668_f3_4	9497	23600	1029	343

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CONTIG3897	26437767_c1_2	9630	23733	294	98															
CONTIG3897	16585912_c2_3	9631	23734	237	79															
CONTIG3897	36330062_c3_4	9632	23735	198	66															
CONTIG3898	29495332_c2_4	9633	23736	219	73															
CONTIG3900	2771010_f2_3	9634	23737	522	174															
CONTIG3902	84650_f3_4	9635	23738	204	68															
CONTIG3902	4511502_c1_8	9636	23739	192	64															
CONTIG3902	26600903_c2_10	9637	23740	201	67															
CONTIG3903	35407805_c3_6	9638	23741	1212	404															
CONTIG3904	33237767_f3_3	9639	23742	273	91															
CONTIG3904	4101561_c2_5	9640	23743	258	86															
CONTIG3905	804151_c3_7	9641	23744	420	140															
CONTIG3907	605078_c2_3	9642	23745	195	65															
CONTIG3908	14562657_f1_1	9643	23746	573	191															
CONTIG3908	24240950_f2_2	9644	23747	1113	371															
CONTIG3908	14507942_f3_3	9645	23748	216	72															
CONTIG3908	6070255_c1_5	9646	23749	273	91															
CONTIG3909	24664641_f1_1	9647	23750	753	251															
CONTIG3909	6734752_f2_2	9648	23751	504	168															
CONTIG3909	26255317_f2_3	9649	23752	594	198															
CONTIG3909	4472502_f3_5	9650	23753	255	85															
CONTIG3911	23594017_c1_4	9651	23754	240	80															
CONTIG3911	4298828_c3_5	9652	23755	219	73															
CONTIG3912	2931377_f1_1	9653	23756	183	61															
CONTIG3912	19729787_f3_2	9654	23757	207	69															
CONTIG3912	22462510_f3_3	9655	23758	225	75															
CONTIG3913	25569552_f3_6	9656	23759	1137	379															
CONTIG3917	3915677_c1_4	9657	23760	216	72															
CONTIG3919	21675305_f2_1	9658	23761	219	73															
CONTIG3919	30156300_f3_3	9659	23762	258	86															
CONTIG3919	470300_c3_7	9660	23763	1116	372															
CONTIG392	35194681_f1_2	9661	23764	219	73															
CONTIG3922	24657885_f2_2	9662	23765	207	69															

CONTIG3922	500010_f3_5	9663	23766	198	66							
CONTIG3922	24407537_c1_6	9664	23767	234	78							
CONTIG3926	878405_f1_1	9665	23768	234	78							
CONTIG3927	22072340_f1_2	9666	23769	831	277							
CONTIG3928	31757160_c2_4	9667	23770	219	73							
CONTIG393	24395207_f3_2	9668	23771	189	63							
CONTIG3932	6140902_f2_2	9669	23772	1188	396							
CONTIG3935	23945430_f2_3	9670	23773	222	74							
CONTIG3935	14566686_c2_7	9671	23774	201	67							
CONTIG3936	32243750_f2_1	9672	23775	195	65							
CONTIG3936	21742000_f3_3	9673	23776	195	65							
CONTIG3936	25475652_f3_4	9674	23777	189	63							
CONTIG3937	23535786_f3_2	9675	23778	252	84							
CONTIG3937	6100628_c2_6	9676	23779	504	168							
CONTIG3938	6140877_f1_2	9677	23780	264	88							
CONTIG394	10734386_f1_2	9678	23781	237	79							
CONTIG394	23835760_f2_3	9679	23782	597	199							
CONTIG3940	5254758_c1_12	9680	23783	237	79							
CONTIG3940	26366506_c1_13	9681	23784	549	183							
CONTIG3940	24823590_c3_14	9682	23785	183	61							
CONTIG3942	209668927_f2_3	9683	23786	285	95							
CONTIG3942	35625000_f3_6	9684	23787	414	138							
CONTIG3943	589160_f1_1	9685	23788	510	170							
CONTIG3943	30507817_c2_4	9686	23789	204	68							
CONTIG3944	23835313_f1_1	9687	23790	258	86							
CONTIG3944	5891430_f2_2	9688	23791	1371	457							
CONTIG395	7054577_f2_1	9689	23792	225	75							
CONTIG395	5908507_c3_3	9690	23793	252	84							
CONTIG3950	29511305_c2_5	9691	23794	240	80							
CONTIG3951	23484662_f3_3	9692	23795	210	70							
CONTIG3953	13313286_c1_5	9693	23796	204	68							
CONTIG3953	188901_c2_6	9694	23797	903	301							
CONTIG3958	12522787_c2_6	9695	23798	480	160							

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CONTIG3983	33770160_c3_6	9729	23832	234	78						
CONTIG3984	15781513_f1_1	9730	23833	192	64						
CONTIG3984	2834561_f2_2	9731	23834	306	102						
CONTIG3984	2117626_f2_4	9732	23835	222	74						
CONTIG3984	9882818_c1_6	9733	23836	993	331						
CONTIG3985	2202_f2_2	9734	23837	990	330						
CONTIG3985	36338443_f3_4	9735	23838	375	125						
CONTIG3985	25394712_c1_10	9736	23839	195	65						
CONTIG3986	1953437_f1_2	9737	23840	189	63						
CONTIG3986	24421915_f1_3	9738	23841	204	68						
CONTIG3986	26382813_c1_8	9739	23842	381	127						
CONTIG3987	24062510_c1_4	9740	23843	186	62						
CONTIG3987	812637_c2_6	9741	23844	213	71						
CONTIG3988	22386538_c1_1	9742	23845	183	61						
CONTIG3988	859807_c1_2	9743	23846	183	61						
CONTIG3989	29945875_f1_1	9744	23847	204	68						
CONTIG3989	656377_c2_3	9745	23848	234	78						
CONTIG399	787660_c1_2	9746	23849	228	76						
CONTIG3990	21991425_f2_1	9747	23850	258	86						
CONTIG3990	24879718_c3_7	9748	23851	1056	352						
CONTIG3991	29487760_f1_1	9749	23852	201	67						
CONTIG3991	4103441_c1_8	9750	23853	195	65						
CONTIG3992	24414188_f1_1	9751	23854	1065	355						
CONTIG3992	23553390_f3_3	9752	23855	240	80						
CONTIG3993	4765656_c1_4	9753	23856	189	63						
CONTIG3993	21683162_c2_7	9754	23857	237	79						
CONTIG3994	4095006_c1_5	9755	23858	279	93						
CONTIG3995	4695177_c1_9	9756	23859	369	123						
CONTIG3995	1350337_c2_11	9757	23860	189	63						
CONTIG3997	25898453_c1_5	9758	23861	474	158						
CONTIG3999	21750003_c1_4	9759	23862	186	62						
CONTIG3999	23641036_c2_5	9760	23863	252	84						
CONTIG4001	36410906_f2_6	9761	23864	204	68						

CONTIG4003	36524037_f2_3	9762	23865	252	84							
CONTIG4005	29878388_f1_2	9763	23866	1014	338							
CONTIG4005	23626952_c2_5	9764	23867	198	66							
CONTIG4005	24255251_c2_6	9765	23868	243	81							
CONTIG4005	20188786_c3_8	9766	23869	333	111							
CONTIG4006	29569562_f2_3	9767	23870	255	85							
CONTIG4006	33210762_c1_5	9768	23871	273	91							
CONTIG4006	5283142_c2_6	9769	23872	1074	358							
CONTIG4007	19730037_c3_7	9770	23873	258	86							
CONTIG4008	25990687_c1_7	9771	23874	186	62							
CONTIG4009	10635927_f1_1	9772	23875	195	65							
CONTIG4009	5111551_f2_4	9773	23876	240	80							
CONTIG4009	4790967_c3_7	9774	23877	231	77							
CONTIG4009	33837903_c3_9	9775	23878	243	81							
CONTIG401	6816555_c3_3	9776	23879	192	64							
CONTIG4010	6817265_f3_1	9777	23880	1263	421							
CONTIG4012	33209687_c3_3	9778	23881	225	75							
CONTIG4013	30275688_c1_2	9779	23882	369	123							
CONTIG4013	14537687_c3_4	9780	23883	204	68							
CONTIG4016	23875885_f2_3	9781	23884	189	63							
CONTIG4016	21695160_f3_6	9782	23885	345	115							
CONTIG4016	3926552_c1_9	9783	23886	558	186							
CONTIG4016	25556700_c2_14	9784	23887	261	87							
CONTIG4016	192052_c3_15	9785	23888	282	94							
CONTIG4017	33407813_f3_5	9786	23889	189	63							
CONTIG402	10725025_c3_2	9787	23890	213	71							
CONTIG4020	6023427_f2_2	9788	23891	279	93							
CONTIG4020	22708393_f3_3	9789	23892	243	81							
CONTIG4020	1970450_c3_5	9790	23893	183	61							
CONTIG4021	24410686_f3_9	9791	23894	243	81							
CONTIG4022	15712778_f1_2	9792	23895	198	66							
CONTIG4024	21729675_c2_5	9793	23896	198	66							
CONTIG4026	24640937_c1_6	9794	23897	441	147							

CONTIG4027	23569437_c1_6	9795	23898	198	66								
CONTIG4029	26570150_c1_6	9796	23899	225	75								
CONTIG403	23609452_f1_1	9797	23900	186	62								
CONTIG403	12269651_f1_2	9798	23901	216	72								
CONTIG403	24429592_c1_3	9799	23902	189	63								
CONTIG4030	22542587_f1_1	9800	23903	246	82								
CONTIG4030	29339678_c1_2	9801	23904	243	81								
CONTIG4030	30109676_c1_3	9802	23905	204	68								
CONTIG4032	3959652_c2_3	9803	23906	549	183								
CONTIG4033	33242877_c2_4	9804	23907	1596	532								
CONTIG4035	5960328_f2_1	9805	23908	240	80								
CONTIG4037	20898387_c3_4	9806	23909	243	81								
CONTIG4038	19585812_f1_1	9807	23910	198	66								
CONTIG4038	16522807_f1_2	9808	23911	876	292								
CONTIG4039	207762_f2_6	9809	23912	243	81								
CONTIG404	204840_f2_2	9810	23913	213	71								
CONTIG4040	20391950_c1_3	9811	23914	225	75								
CONTIG4041	23479753_f1_1	9812	23915	240	80								
CONTIG4041	4381307_f1_2	9813	23916	216	72								
CONTIG4042	6768753_f3_3	9814	23917	258	86								
CONTIG4042	821925_f3_4	9815	23918	186	62								
CONTIG4042	19173313_c3_7	9816	23919	1317	439								
CONTIG4043	13756250_f3_3	9817	23920	279	93								
CONTIG4043	860015_c3_7	9818	23921	204	68								
CONTIG4044	26641533_c2_4	9819	23922	222	74								
CONTIG4045	12766918_f3_4	9820	23923	204	68								
CONTIG4045	34258387_f3_5	9821	23924	222	74								
CONTIG4045	2464178_c2_9	9822	23925	189	63								
CONTIG4047	35804715_f2_4	9823	23926	249	83								
CONTIG4047	33204068_c3_7	9824	23927	285	95								
CONTIG4048	23444001_c3_4	9825	23928	198	66								
CONTIG4053	24039140_f2_1	9826	23929	237	79								
CONTIG4053	29533143_f2_3	9827	23930	288	96								

CONTIG4055	24657687_c1_6	9828	23931	1515	505								
CONTIG4056	30179516_c2_6	9829	23932	249	83								
CONTIG4057	4485062_f1_1	9830	23933	222	74								
CONTIG4057	9875292_c3_6	9831	23934	198	66								
CONTIG4057	23475050_c3_7	9832	23935	1266	422								
CONTIG4058	29334787_f2_1	9833	23936	501	167								
CONTIG4058	4767503_f2_2	9834	23937	1473	491								
CONTIG4058	30475887_f3_3	9835	23938	375	125								
CONTIG4059	12932067_c2_3	9836	23939	183	61								
CONTIG406	6818926_f1_1	9837	23940	231	77								
CONTIG4061	9772143_f2_5	9838	23941	234	78								
CONTIG4062	25876680_c1_5	9839	23942	204	68								
CONTIG4062	20580275_c3_8	9840	23943	237	79								
CONTIG4063	5250252_f3_4	9841	23944	366	122								
CONTIG4063	24410887_c2_5	9842	23945	255	85								
CONTIG4063	30751563_c3_6	9843	23946	216	72								
CONTIG4066	204088_f2_1	9844	23947	246	82								
CONTIG4067	20425776_f1_1	9845	23948	234	78								
CONTIG4067	34554013_c3_7	9846	23949	288	96								
CONTIG4068	5260903_f3_2	9847	23950	228	76								
CONTIG4068	23939062_c2_4	9848	23951	231	77								
CONTIG4069	16798428_f1_2	9849	23952	183	61								
CONTIG4069	2188800_f2_3	9850	23953	255	85								
CONTIG4069	23626536_c2_7	9851	23954	183	61								
CONTIG4069	34573462_c2_8	9852	23955	273	91								
CONTIG4072	4976587_c1_10	9853	23956	195	65								
CONTIG4073	22351551_f2_1	9854	23957	192	64								
CONTIG4073	19537512_c1_2	9855	23958	1269	423								
CONTIG4075	970392_f1_2	9856	23959	228	76								
CONTIG4075	12502251_c2_12	9857	23960	192	64								
CONTIG4075	13863808_c2_13	9858	23961	225	75								
CONTIG4076	657530_c3_6	9859	23962	1164	388								
CONTIG4078	782965_c1_6	9860	23963	1335	445								





CONTIG4105	22476512_c2_8	9894	23997	225	75
CONTIG4107	4797155_c1_3	9895	23998	372	124
CONTIG4108	23926683_f2_4	9896	23999	246	82
CONTIG4108	26570458_f3_6	9897	24000	189	63
CONTIG4108	2783400_c1_8	9898	24001	201	67
CONTIG4109	25582682_f2_4	9899	24002	228	76
CONTIG4109	31532167_c1_5	9900	24003	243	81
CONTIG4112	4797752_c3_5	9901	24004	186	62
CONTIG4115	4460135_f3_2	9902	24005	183	61
CONTIG4116	24413883_f2_1	9903	24006	378	126
CONTIG4118	25661042_c1_8	9904	24007	1431	477
CONTIG4119	23941927_f3_1	9905	24008	720	240
CONTIG4119	16500_c1_2	9906	24009	237	79
CONTIG4119	25672215_c3_5	9907	24010	186	62
CONTIG412	585002_f3_1	9908	24011	321	107
CONTIG4120	4890693_f2_3	9909	24012	240	80
CONTIG4120	5898400_f3_4	9910	24013	525	175
CONTIG4121	4335312_f1_1	9911	24014	189	63
CONTIG4121	26203388_f1_2	9912	24015	927	309
CONTIG4121	176538_f3_4	9913	24016	204	68
CONTIG4123	23859437_f1_1	9914	24017	186	62
CONTIG4123	2402078_f3_3	9915	24018	183	61
CONTIG4123	4179708_f3_4	9916	24019	183	61
CONTIG4124	26350001_f2_3	9917	24020	411	137
CONTIG4125	30157938_f2_5	9918	24021	192	64
CONTIG4126	22460012_c2_7	9919	24022	396	132
CONTIG4127	22270931_f2_2	9920	24023	576	192
CONTIG4127	135906_c3_6	9921	24024	288	96
CONTIG4128	978575_f2_2	9922	24025	783	261
CONTIG4128	187507_c1_7	9923	24026	255	85
CONTIG4128	25438431_c3_8	9924	24027	456	152
CONTIG4130	31367137_f1_3	9925	24028	183	61
CONTIG4131	12610660_c2_9	9926	24029	183	61

CONTIG4133	3917078_f1_2	9927	24030	204	68
CONTIG4133	1954385_f1_3	9928	24031	246	82
CONTIG4133	20317067_f2_4	9929	24032	195	65
CONTIG4133	35647042_c2_6	9930	24033	189	63
CONTIG4134	14063127_f2_1	9931	24034	933	311
CONTIG4134	175011_f3_4	9932	24035	762	254
CONTIG4134	6697302_c2_6	9933	24036	234	78
CONTIG4135	30573550_f1_3	9934	24037	183	61
CONTIG4135	22268763_c1_5	9935	24038	312	104
CONTIG4135	10945277_c1_6	9936	24039	213	71
CONTIG4135	4150912_c1_7	9937	24040	249	83
CONTIG4139	10019187_c2_10	9938	24041	1143	381
CONTIG4140	14860306_c1_5	9939	24042	348	116
CONTIG4142	34173513_c3_4	9940	24043	705	235
CONTIG4145	970087_f1_1	9941	24044	291	97
CONTIG4145	502290_f2_2	9942	24045	603	201
CONTIG4145	15641627_c3_8	9943	24046	240	80
CONTIG4146	24411052_c2_8	9944	24047	573	191
CONTIG4146	33439635_c3_9	9945	24048	189	63
CONTIG4147	2937750_c3_7	9946	24049	528	176
CONTIG4148	14647177_f1_1	9947	24050	189	63
CONTIG4148	197655_f3_3	9948	24051	276	92
CONTIG415	4898411_c3_6	9949	24052	273	91
CONTIG4150	10423577_f2_4	9950	24053	189	63
CONTIG4150	910905_c1_12	9951	24054	339	113
CONTIG4151	22298177_f1_1	9952	24055	204	68
CONTIG4151	36620465_c1_5	9953	24056	207	69
CONTIG4152	16531300_f2_4	9954	24057	306	102
CONTIG4152	25392127_f2_5	9955	24058	240	80
CONTIG4153	24250017_f3_2	9956	24059	1317	439
CONTIG4154	23553887_c1_5	9957	24060	282	94
CONTIG4155	4806883_f2_1	9958	24061	240	80
CONTIG4155	43183333_c3_4	9959	24062	192	64

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CONTIG4227	25391316_c2_7	10059	24162	222	74
CONTIG4228	34610255_f3_6	10060	24163	807	269
CONTIG4228	30111343_c1_7	10061	24164	207	69
CONTIG4229	4710761_f2_1	10062	24165	462	154
CONTIG423	23679677_f2_1	10063	24166	201	67
CONTIG423	22297187_c3_2	10064	24167	216	72
CONTIG4230	3944692_f1_1	10065	24168	576	192
CONTIG4232	23540676_f1_3	10066	24169	210	70
CONTIG4232	4721408_f2_4	10067	24170	186	62
CONTIG4233	23867002_c1_2	10068	24171	828	276
CONTIG4233	10554750_c3_6	10069	24172	213	71
CONTIG4235	867775_f3_5	10070	24173	207	69
CONTIG4235	24020285_c3_7	10071	24174	240	80
CONTIG4236	47137_c2_5	10072	24175	1452	484
CONTIG4237	24398505_c1_4	10073	24176	213	71
CONTIG4237	11204691_c1_6	10074	24177	246	82
CONTIG4239	13085917_f3_3	10075	24178	210	70
CONTIG4239	15819062_c2_4	10076	24179	186	62
CONTIG4239	12772677_c3_5	10077	24180	240	80
CONTIG4240	33595882_c3_3	10078	24181	195	65
CONTIG4241	4101075_c2_7	10079	24182	183	61
CONTIG4241	34581257_c2_9	10080	24183	186	62
CONTIG4241	26367212_c3_11	10081	24184	204	68
CONTIG4242	5469035_f1_2	10082	24185	180	60
CONTIG4242	11963542_f3_4	10083	24186	315	105
CONTIG4242	33241625_f3_5	10084	24187	210	70
CONTIG4243	988252_c1_4	10085	24188	216	72
CONTIG4244	21991530_f1_1	10086	24189	402	134
CONTIG4244	24798193_f2_2	10087	24190	213	71
CONTIG4244	13866682_f3_4	10088	24191	216	72
CONTIG4244	25564812_c1_7	10089	24192	246	82
CONTIG4244	14459525_c3_13	10090	24193	183	61
CONTIG4245	26672055_f2_4	10091	24194	189	63

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CONTIG4266	36074156_c2_5	10125	24228	231	77
CONTIG4268	22078517_c2_9	10126	24229	201	67
CONTIG4269	25664001_c1_2	10127	24230	219	73
CONTIG427	423261_f2_1	10128	24231	378	126
CONTIG427	24300006_c2_3	10129	24232	243	81
CONTIG4271	401655_f3_5	10130	24233	195	65
CONTIG4271	35188825_c2_6	10131	24234	195	65
CONTIG4272	32063462_c1_4	10132	24235	726	242
CONTIG4273	32531558_c1_8	10133	24236	828	276
CONTIG4273	9765628_c3_11	10134	24237	1017	339
CONTIG4274	23537831_c2_9	10135	24238	192	64
CONTIG4275	13859626_c1_6	10136	24239	1182	394
CONTIG4275	6250305_c3_8	10137	24240	225	75
CONTIG4278	1368877_f2_3	10138	24241	192	64
CONTIG4278	35399086_f3_4	10139	24242	186	62
CONTIG428	19620463_c1_4	10140	24243	186	62
CONTIG4282	4896927_c1_7	10141	24244	234	78
CONTIG4283	21932625_f2_2	10142	24245	363	121
CONTIG4283	35676576_f3_3	10143	24246	537	179
CONTIG4283	20351625_c3_12	10144	24247	450	150
CONTIG4284	15625458_f2_2	10145	24248	219	73
CONTIG4284	3927_f3_4	10146	24249	195	65
CONTIG4284	20365825_c1_5	10147	24250	192	64
CONTIG4285	24306588_f3_2	10148	24251	207	69
CONTIG4285	23648937_c2_7	10149	24252	273	91
CONTIG4285	10631250_c2_8	10150	24253	210	70
CONTIG4287	11807825_f2_3	10151	24254	237	79
CONTIG4287	4187830_c2_9	10152	24255	528	176
CONTIG4288	9846900_f1_1	10153	24256	204	68
CONTIG4288	19926260_c2_5	10154	24257	201	67
CONTIG4289	12782393_f3_3	10155	24258	237	79
CONTIG4289	15888_c2_6	10156	24259	222	74
CONTIG429	29456300_c1_2	10157	24260	360	120

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CONTIG4551	814457_f3_7	10488	24591	186	62								
CONTIG4552	2566607_f3_10	10489	24592	195	65								
CONTIG4552	33699002_c1_11	10490	24593	207	69								
CONTIG4552	9954032_c2_15	10491	24594	642	214								
CONTIG4554	29296893_f1_1	10492	24595	627	209								
CONTIG4554	23469081_f2_4	10493	24596	231	77								
CONTIG4556	1211516_f3_6	10494	24597	234	78								
CONTIG4556	30581500_c2_8	10495	24598	204	68								
CONTIG4557	5086537_c2_8	10496	24599	279	93								
CONTIG4558	6913151_f1_1	10497	24600	1023	341								
CONTIG4558	16447213_f3_5	10498	24601	195	65								
CONTIG4560	5360192_f3_3	10499	24602	414	138								
CONTIG4561	24239061_f2_2	10500	24603	201	67								
CONTIG4561	13675252_f2_4	10501	24604	207	69								
CONTIG4565	21722756_c2_6	10502	24605	375	125								
CONTIG4565	24800877_c3_7	10503	24606	627	209								
CONTIG4566	24666067_f1_1	10504	24607	231	77								
CONTIG4567	22070286_f2_1	10505	24608	216	72								
CONTIG4568	4740717_f1_1	10506	24609	237	79								
CONTIG4568	22539075_c2_8	10507	24610	1062	354								
CONTIG4568	13883577_c3_9	10508	24611	270	90								
CONTIG4569	11877175_f3_2	10509	24612	273	91								
CONTIG4569	12383582_c3_6	10510	24613	183	61								
CONTIG4569	24665927_c3_7	10511	24614	411	137								
CONTIG4571	24218753_f1_1	10512	24615	195	65								
CONTIG4571	7986052_c1_4	10513	24616	186	62								
CONTIG4572	213535_f3_2	10514	24617	270	90								
CONTIG4572	29692680_c2_3	10515	24618	183	61								
CONTIG4572	3004843_c2_4	10516	24619	183	61								
CONTIG4574	31287811_c1_6	10517	24620	210	70								
CONTIG4575	3907677_c1_5	10518	24621	255	85								
CONTIG4575	23835952_c3_10	10519	24622	456	152								
CONTIG4576	4073552_f2_5	10520	24623	246	82								



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CONTIG4885	4694003_f3_7	11016	25119	228	76
CONTIG4887	9776015_f3_2	11017	25120	282	94
CONTIG4887	24391068_c2_4	11018	25121	192	64
CONTIG4887	430375_c2_5	11019	25122	192	64
CONTIG4888	14197175_f2_2	11020	25123	192	64
CONTIG4890	35890_c1_6	11021	25124	225	75
CONTIG4891	22945260_f1_1	11022	25125	333	111
CONTIG4891	2745927_f2_3	11023	25126	207	69
CONTIG4891	31662753_f2_4	11024	25127	192	64
CONTIG4891	10164181_f3_6	11025	25128	243	81
CONTIG4897	24610777_c2_4	11026	25129	390	130
CONTIG4898	4354543_f2_2	11027	25130	183	61
CONTIG4898	24025012_c2_5	11028	25131	249	83
CONTIG49	4179708_f1_1	11029	25132	183	61
CONTIG4900	10738777_f2_5	11030	25133	642	214
CONTIG4900	29845302_c2_9	11031	25134	240	80
CONTIG4901	25444067_c2_7	11032	25135	207	69
CONTIG4903	20115885_f2_2	11033	25136	189	63
CONTIG4903	31284425_f3_4	11034	25137	807	269
CONTIG4906	35207811_f2_2	11035	25138	186	62
CONTIG4906	35205406_f2_3	11036	25139	189	63
CONTIG4906	21520125_c1_7	11037	25140	837	279
CONTIG4908	36148255_c2_7	11038	25141	249	83
CONTIG4908	9876290_c2_8	11039	25142	300	100
CONTIG4908	251260_c2_9	11040	25143	291	97
CONTIG4908	10721901_c3_10	11041	25144	195	65
CONTIG4909	25990699_c1_5	11042	25145	189	63
CONTIG4910	20501562_c2_3	11043	25146	696	232
CONTIG4910	5913913_c2_4	11044	25147	237	79
CONTIG4911	275458_f2_1	11045	25148	207	69
CONTIG4911	2929003_c1_10	11046	25149	198	66
CONTIG4911	24410808_c3_15	11047	25150	474	158
CONTIG4912	9865757_c1_4	11048	25151	354	118

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CONTIG4979	5276587_c2_15	11148	25251	312	104
CONTIG4980	22381952_c1_6	11149	25252	231	77
CONTIG4981	34085160_f2_1	11150	25253	210	70
CONTIG4981	24417313_f3_2	11151	25254	321	107
CONTIG4981	23626302_f3_5	11152	25255	195	65
CONTIG4981	14301280_c1_7	11153	25256	219	73
CONTIG4981	19789036_c2_8	11154	25257	255	85
CONTIG4982	24414062_c1_12	11155	25258	222	74
CONTIG4982	34272145_c2_13	11156	25259	558	186
CONTIG4983	1073317_f2_5	11157	25260	228	76
CONTIG4984	36366307_c3_11	11158	25261	423	141
CONTIG4985	14860718_f1_1	11159	25262	276	92
CONTIG4985	30119627_f3_4	11160	25263	1566	522
CONTIG4986	24422762_f1_1	11161	25264	453	151
CONTIG4986	11912502_f2_3	11162	25265	195	65
CONTIG4987	26252187_c1_5	11163	25266	195	65
CONTIG4988	25447182_f3_3	11164	25267	186	62
CONTIG4988	4147343_c1_5	11165	25268	297	99
CONTIG4989	20501302_f2_2	11166	25269	198	66
CONTIG4989	2047528_c2_5	11167	25270	909	303
CONTIG4990	23601535_f2_5	11168	25271	876	292
CONTIG4990	34251636_f3_6	11169	25272	183	61
CONTIG4991	22301250_f2_2	11170	25273	204	68
CONTIG4993	9929563_f3_4	11171	25274	198	66
CONTIG4993	33398427_c1_6	11172	25275	342	114
CONTIG4994	21898450_c2_7	11173	25276	648	216
CONTIG4995	4156331_f2_1	11174	25277	189	63
CONTIG4995	19585265_f2_2	11175	25278	429	143
CONTIG4995	12895128_c1_4	11176	25279	252	84
CONTIG4995	4937801_c2_6	11177	25280	240	80
CONTIG4995	14660261_c2_8	11178	25281	198	66
CONTIG4996	26369053_f2_2	11179	25282	186	62
CONTIG4996	5313388_c3_12	11180	25283	186	62





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CONTIGS034	13759413_f1_1	11247	25350	891	297
CONTIGS034	22690937_c1_10	11248	25351	267	89
CONTIGS035	30182642_f2_7	11249	25352	207	69
CONTIGS035	4377313_c2_12	11250	25353	216	72
CONTIGS035	3989012_c2_13	11251	25354	708	236
CONTIGS036	14098402_f3_6	11252	25355	231	77
CONTIGS036	36360938_c1_7	11253	25356	228	76
CONTIGS036	21507678_c2_9	11254	25357	354	118
CONTIGS037	23649063_c2_6	11255	25358	246	82
CONTIGS039	14254667_c1_4	11256	25359	366	122
CONTIGS04	29339805_c1_4	11257	25360	195	65
CONTIGS04	29493785_c2_5	11258	25361	270	90
CONTIGS040	191566_f1_1	11259	25362	258	86
CONTIGS040	431557_f3_5	11260	25363	345	115
CONTIGS041	26772325_f2_2	11261	25364	894	298
CONTIGS041	36132217_c3_15	11262	25365	651	217
CONTIGS042	20320311_f3_4	11263	25366	201	67
CONTIGS042	402257_c3_10	11264	25367	2025	675
CONTIGS043	34156500_c1_8	11265	25368	243	81
CONTIGS044	23875627_f1_1	11266	25369	1329	443
CONTIGS044	20354510_c2_5	11267	25370	216	72
CONTIGS047	6095640_f3_5	11268	25371	234	78
CONTIGS049	23478181_f3_7	11269	25372	243	81
CONTIGS05	35425831_f3_1	11270	25373	876	292
CONTIGS050	6267_c1_4	11271	25374	279	93
CONTIGS050	20876512_c3_7	11272	25375	294	98
CONTIGS050	10970287_c3_8	11273	25376	201	67
CONTIGS051	22863265_c3_10	11274	25377	267	89
CONTIGS052	30079093_f1_1	11275	25378	807	269
CONTIGS052	23626265_c3_6	11276	25379	192	64
CONTIGS053	23907900_f3_5	11277	25380	204	68
CONTIGS054	431275_f2_3	11278	25381	210	70
CONTIGS054	25397687_c2_9	11279	25382	837	279

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CONTIG507	14063177_c1_2	11313	25416	195	65				
CONTIG5070	4765876_c1_5	11314	25417	204	68				
CONTIG5070	30089376_c2_7	11315	25418	288	96				
CONTIG5070	35943812_c2_8	11316	25419	213	71				
CONTIG5071	4157777_c2_10	11317	25420	1056	352				
CONTIG5072	198403_f1_2	11318	25421	270	90				
CONTIG5073	2914762_f2_1	11319	25422	198	66				
CONTIG5073	4506876_f3_3	11320	25423	852	284				
CONTIG5073	5890640_c1_4	11321	25424	294	98				
CONTIG5073	24485688_c1_5	11322	25425	267	89				
CONTIG5073	20703160_c1_6	11323	25426	1368	456				
CONTIG5073	164061_c1_7	11324	25427	1107	369				
CONTIG5074	26305442_c2_8	11325	25428	192	64				
CONTIG5075	24428212_c1_5	11326	25429	201	67				
CONTIG5077	4117752_f2_1	11327	25430	183	61				
CONTIG5077	32206260_f3_4	11328	25431	192	64				
CONTIG5077	14140966_c3_8	11329	25432	270	90				
CONTIG5078	7032942_c2_10	11330	25433	201	67				
CONTIG5080	1367202_f3_8	11331	25434	276	92				
CONTIG5080	119017_c1_11	11332	25435	432	144				
CONTIG5080	34008282_c3_15	11333	25436	219	73				
CONTIG5081	24016517_f3_3	11334	25437	213	71				
CONTIG5081	16204531_c2_8	11335	25438	237	79				
CONTIG5082	4454651_f2_5	11336	25439	237	79				
CONTIG5083	550627_f1_1	11337	25440	312	104				
CONTIG5083	4898250_f3_5	11338	25441	1932	644				
CONTIG5083	35163150_c1_6	11339	25442	195	65				
CONTIG5083	1046900_c2_7	11340	25443	219	73				
CONTIG5083	4485950_c3_10	11341	25444	480	160				
CONTIG5084	15740888_f1_3	11342	25445	465	155				
CONTIG5085	24657875_c3_11	11343	25446	213	71				
CONTIG5086	4187626_c3_6	11344	25447	261	87				
CONTIG5087	23906256_c1_6	11345	25448	219	73				

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CONTIGS155	4069761_c1_10	11478	25581	183	61
CONTIGS155	30110812_c2_15	11479	25582	183	61
CONTIGS155	21525062_c2_16	11480	25583	207	69
CONTIGS155	23602002_c3_19	11481	25584	306	102
CONTIGS157	600880_f1_1	11482	25585	291	97
CONTIGS157	30267632_f3_3	11483	25586	183	61
CONTIGS157	22382755_c2_7	11484	25587	306	102
CONTIGS157	21729061_c3_11	11485	25588	222	74
CONTIGS158	25991031_f3_5	11486	25589	195	65
CONTIGS158	22477187_f3_6	11487	25590	183	61
CONTIGS159	24805261_f1_1	11488	25591	204	68
CONTIGS16	19563908_c2_1	11489	25592	198	66
CONTIGS160	7080077_f3_7	11490	25593	204	68
CONTIGS163	3907512_c2_6	11491	25594	207	69
CONTIGS164	14495325_c1_8	11492	25595	195	65
CONTIGS164	21722002_c2_11	11493	25596	201	67
CONTIGS165	26253375_f1_1	11494	25597	186	62
CONTIGS166	3930_f1_1	11495	25598	303	101
CONTIGS168	22464057_f2_6	11496	25599	255	85
CONTIGS169	196926_f3_6	11497	25600	978	326
CONTIGS17	30350276_f2_2	11498	25601	216	72
CONTIGS171	20323306_f3_6	11499	25602	405	135
CONTIGS171	26207682_c1_8	11500	25603	240	80
CONTIGS171	2922505_c2_10	11501	25604	207	69
CONTIGS172	4881300_f3_4	11502	25605	270	90
CONTIGS173	164018_c1_3	11503	25606	201	67
CONTIGS176	16415952_c1_5	11504	25607	192	64
CONTIGS178	6662691_f1_1	11505	25608	195	65
CONTIGS179	390950_f1_3	11506	25609	363	121
CONTIGS179	12207757_f1_4	11507	25610	210	70
CONTIGS179	987625_f1_5	11508	25611	240	80
CONTIGS179	29923502_f2_7	11509	25612	243	81
CONTIGS179	5866382_c2_17	11510	25613	348	116



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CONTIG5323	2953375_c3_12	11808	25911	2118	706															
CONTIG5324	6433177_f1_3	11809	25912	186	62															
CONTIG5324	7039075_c2_14	11810	25913	201	67															
CONTIG5325	23479805_f1_2	11811	25914	255	85															
CONTIG5327	33398258_c1_6	11812	25915	204	68															
CONTIG5329	9850182_f3_4	11813	25916	201	67															
CONTIG5329	22037675_c1_9	11814	25917	576	192															
CONTIG533	24335910_f3_2	11815	25918	267	89															
CONTIG5330	16209687_f1_1	11816	25919	198	66															
CONTIG5330	16853135_f3_5	11817	25920	198	66															
CONTIG5330	24234753_c1_9	11818	25921	264	88															
CONTIG5330	14584763_c1_11	11819	25922	237	79															
CONTIG5330	683215_c2_12	11820	25923	192	64															
CONTIG5330	5261580_c3_14	11821	25924	222	74															
CONTIG5331	21878465_f1_1	11822	25925	381	127															
CONTIG5331	24251900_c1_6	11823	25926	195	65															
CONTIG5331	198813_c2_8	11824	25927	849	283															
CONTIG5334	429561_c2_9	11825	25928	204	68															
CONTIG5335	3937510_f2_2	11826	25929	1095	365															
CONTIG5335	31250052_c3_11	11827	25930	225	75															
CONTIG5336	1174007_f2_5	11828	25931	192	64															
CONTIG5336	26213413_f3_8	11829	25932	228	76															
CONTIG5336	20428386_c1_11	11830	25933	483	161															
CONTIG5338	24414062_f1_1	11831	25934	267	89															
CONTIG5338	24417630_f3_6	11832	25935	189	63															
CONTIG5338	14485250_c1_8	11833	25936	183	61															
CONTIG5338	6024051_c3_11	11834	25937	186	62															
CONTIG5339	907201_f2_3	11835	25938	183	61															
CONTIG5339	1984577_f2_5	11836	25939	210	70															
CONTIG5339	515777_c3_10	11837	25940	339	113															
CONTIG534	33365876_f2_1	11838	25941	306	102															
CONTIG534	9820132_c2_5	11839	25942	270	90															
CONTIG5340	12523392_f2_2	11840	25943	546	182															

CONTIG5341	33781505_f2_8	11841	25944	261	87				
CONTIG5342	13912633_f1_2	11842	25945	246	82				
CONTIG5343	14548186_c2_18	11843	25946	216	72				
CONTIG5343	5125007_c3_26	11844	25947	531	177				
CONTIG5344	56313_f1_3	11845	25948	192	64				
CONTIG5344	34117307_f1_5	11846	25949	267	89				
CONTIG5345	10286263_f2_6	11847	25950	192	64				
CONTIG5345	5115642_c1_18	11848	25951	465	155				
CONTIG5346	29704625_c1_8	11849	25952	249	83				
CONTIG5347	33619527_c2_10	11850	25953	2040	680				
CONTIG5348	3126963_f3_8	11851	25954	216	72				
CONTIG5349	13783200_f1_1	11852	25955	249	83				
CONTIG5349	16797050_c1_8	11853	25956	198	66				
CONTIG5349	15705627_c1_9	11854	25957	225	75				
CONTIG5349	426402_c3_11	11855	25958	195	65				
CONTIG535	20894667_f2_1	11856	25959	270	90				
CONTIG5350	10162937_f1_4	11857	25960	183	61				
CONTIG5350	1172175_f2_8	11858	25961	528	176				
CONTIG5351	10938836_f1_1	11859	25962	240	80				
CONTIG5352	6757750_f2_1	11860	25963	240	80				
CONTIG5352	6820182_c1_6	11861	25964	255	85				
CONTIG5352	26192052_c3_11	11862	25965	258	86				
CONTIG5353	2741638_c1_12	11863	25966	183	61				
CONTIG5353	24015902_c3_16	11864	25967	606	202				
CONTIG5356	33788386_f1_1	11865	25968	519	173				
CONTIG5356	13682930_f3_3	11866	25969	201	67				
CONTIG5356	4172755_c2_8	11867	25970	186	62				
CONTIG5357	4820392_f1_4	11868	25971	243	81				
CONTIG5357	125300_f2_5	11869	25972	201	67				
CONTIG5357	5116557_c1_16	11870	25973	1119	373				
CONTIG5358	4117313_c2_11	11871	25974	189	63				
CONTIG5359	11756937_c3_16	11872	25975	819	273				
CONTIG536	33619125_c2_4	11873	25976	273	91				

CONTIG5360	4037512_f2_4	11874	25977	258	86
CONTIG5360	29301028_c2_11	11875	25978	276	92
CONTIG5360	13798305_c3_13	11876	25979	279	93
CONTIG5361	6439076_f2_2	11877	25980	255	85
CONTIG5361	29486285_c3_10	11878	25981	201	67
CONTIG5361	4886292_c3_12	11879	25982	423	141
CONTIG5361	23687507_c3_14	11880	25983	204	68
CONTIG5362	21892038_f2_6	11881	25984	300	100
CONTIG5363	29463528_f2_5	11882	25985	267	89
CONTIG5363	23629158_f2_11	11883	25986	201	67
CONTIG5363	20345053_c1_20	11884	25987	183	61
CONTIG5363	22556636_c2_23	11885	25988	267	89
CONTIG5364	21929082_f2_6	11886	25989	240	80
CONTIG5365	24485937_f1_2	11887	25990	285	95
CONTIG5365	158125_f2_9	11888	25991	183	61
CONTIG5366	30268887_c3_8	11889	25992	201	67
CONTIG5367	24410890_f3_8	11890	25993	243	81
CONTIG5368	1050638_f2_3	11891	25994	270	90
CONTIG5368	6726411_c1_9	11892	25995	351	117
CONTIG5368	30516952_c2_12	11893	25996	192	64
CONTIG5368	523276_c3_18	11894	25997	273	91
CONTIG5369	6015682_c3_9	11895	25998	552	184
CONTIG537	290627_c2_1	11896	25999	189	63
CONTIG5370	30157932_f1_1	11897	26000	357	119
CONTIG5370	14142586_f2_3	11898	26001	213	71
CONTIG5370	4730267_c1_10	11899	26002	432	144
CONTIG5371	4417152_c1_14	11900	26003	222	74
CONTIG5371	13870187_c3_21	11901	26004	309	103
CONTIG5372	109400_f2_7	11902	26005	363	121
CONTIG5372	1985312_f3_11	11903	26006	195	65
CONTIG5372	20115892_c3_18	11904	26007	291	97
CONTIG5373	6567_c2_7	11905	26008	588	196
CONTIG5373	13789062_c2_8	11906	26009	231	77

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CONTIGS422	11718750_c1_14	12039	26142	204	68						
CONTIGS422	22538175_c3_22	12040	26143	315	105						
CONTIGS423	14876550_f1_1	12041	26144	2082	694						
CONTIGS424	13781556_f3_2	12042	26145	621	207						
CONTIGS424	125701_c3_13	12043	26146	186	62						
CONTIGS424	16803817_c3_14	12044	26147	219	73						
CONTIGS425	19776928_f1_2	12045	26148	207	69						
CONTIGS426	5256587_f2_3	12046	26149	285	95						
CONTIGS426	31365640_f3_5	12047	26150	300	100						
CONTIGS426	12895275_c2_11	12048	26151	210	70						
CONTIGS427	24392052_f1_2	12049	26152	192	64						
CONTIGS427	5984437_f3_4	12050	26153	234	78						
CONTIGS427	3392056_f3_12	12051	26154	195	65						
CONTIGS429	22275128_f1_1	12052	26155	1329	443						
CONTIGS429	25426680_c1_7	12053	26156	297	99						
CONTIGS429	21881886_c1_8	12054	26157	183	61						
CONTIGS429	24220286_c3_10	12055	26158	195	65						
CONTIGS429	20757886_c3_11	12056	26159	234	78						
CONTIGS43	12312692_f2_1	12057	26160	645	215						
CONTIGS43	21759677_f3_2	12058	26161	258	86						
CONTIGS430	14102176_c1_14	12059	26162	900	300						
CONTIGS430	23704776_c1_15	12060	26163	300	100						
CONTIGS431	5914078_f2_5	12061	26164	222	74						
CONTIGS431	2734755_c2_11	12062	26165	195	65						
CONTIGS432	24789826_f2_9	12063	26166	273	91						
CONTIGS432	22460937_c1_16	12064	26167	366	122						
CONTIGS433	32120177_f3_5	12065	26168	255	85						
CONTIGS433	1179165_c3_13	12066	26169	207	69						
CONTIGS434	23475782_f1_2	12067	26170	237	79						
CONTIGS434	48402_c3_8	12068	26171	246	82						
CONTIGS434	14636505_c3_9	12069	26172	201	67						
CONTIGS434	26345277_c3_10	12070	26173	642	214						
CONTIGS435	33440715_f3_5	12071	26174	192	64						





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CONTIG5501	21567912_c2_29	12237	26340	210	70						
CONTIG5502	3954050_f2_3	12238	26341	189	63						
CONTIG5503	253_f1_3	12239	26342	678	226						
CONTIG5504	20508287_f3_6	12240	26343	396	132						
CONTIG5504	7203187_c1_12	12241	26344	213	71						
CONTIG5504	3320306_c3_18	12242	26345	1239	413						
CONTIG5504	20881252_c3_19	12243	26346	219	73						
CONTIG5505	25553507_f1_3	12244	26347	216	72						
CONTIG5505	2535686_f2_5	12245	26348	264	88						
CONTIG5505	11110911_c2_11	12246	26349	420	140						
CONTIG5505	23913202_c2_12	12247	26350	267	89						
CONTIG5506	34078537_f1_3	12248	26351	318	106						
CONTIG5506	781287_f2_4	12249	26352	261	87						
CONTIG5506	4162503_c1_11	12250	26353	678	226						
CONTIG5506	32147552_c1_12	12251	26354	219	73						
CONTIG5507	15656250_f1_3	12252	26355	204	68						
CONTIG5507	781302_f1_4	12253	26356	201	67						
CONTIG5507	22265677_c2_14	12254	26357	183	61						
CONTIG5508	32693806_f1_1	12255	26358	408	136						
CONTIG5508	14456325_c1_21	12256	26359	654	218						
CONTIG5509	4960932_f1_1	12257	26360	255	85						
CONTIG5509	32037837_f2_4	12258	26361	306	102						
CONTIG5509	26214161_f3_5	12259	26362	330	110						
CONTIG5509	22709818_c1_7	12260	26363	201	67						
CONTIG5509	13860887_c2_11	12261	26364	231	77						
CONTIG5509	4805438_c2_12	12262	26365	204	68						
CONTIG551	25437800_c3_3	12263	26366	198	66						
CONTIG5510	4766927_f1_6	12264	26367	207	69						
CONTIG5510	2458437_f3_11	12265	26368	252	84						
CONTIG5510	4790903_f3_13	12266	26369	753	251						
CONTIG5510	6362505_c2_18	12267	26370	201	67						
CONTIG5511	25449187_f1_1	12268	26371	297	99						
CONTIG5511	20317_f1_2	12269	26372	186	62						

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CONTIGS591	24414052_c2_11	12501	26604	228	76
CONTIGS592	10585378_c2_5	12502	26605	609	203
CONTIGS592	20086015_c3_7	12503	26606	213	71
CONTIGS592	33985002_c3_9	12504	26607	678	226
CONTIGS593	4885841_f1_1	12505	26608	327	109
CONTIGS593	23629403_f3_6	12506	26609	189	63
CONTIGS593	4818931_f3_10	12507	26610	183	61
CONTIGS593	629682_c2_16	12508	26611	285	95
CONTIGS593	21539032_c3_20	12509	26612	840	280
CONTIGS594	4891577_f2_4	12510	26613	279	93
CONTIGS594	21759702_c1_13	12511	26614	195	65
CONTIGS594	4865878_c3_18	12512	26615	183	61
CONTIGS595	21663931_c2_8	12513	26616	978	326
CONTIGS595	986025_c3_13	12514	26617	1101	367
CONTIGS596	14586530_f1_5	12515	26618	1023	341
CONTIGS596	23410_f3_13	12516	26619	249	83
CONTIGS596	894437_c2_17	12517	26620	333	111
CONTIGS597	24023587_f3_8	12518	26621	192	64
CONTIGS598	589717_f1_1	12519	26622	231	77
CONTIGS598	20322767_f2_6	12520	26623	183	61
CONTIGS598	24511068_f2_10	12521	26624	540	180
CONTIGS598	15085765_f3_11	12522	26625	207	69
CONTIGS598	16144783_f3_14	12523	26626	213	71
CONTIGS598	11757300_c3_25	12524	26627	195	65
CONTIGS599	29945875_f1_2	12525	26628	204	68
CONTIGS599	20709436_f2_6	12526	26629	267	89
CONTIGS599	23925017_c1_13	12527	26630	1179	393
CONTIGS599	11900015_c2_15	12528	26631	195	65
CONTIGS599	4485055_c3_17	12529	26632	186	62
CONTIGS600	7031938_f1_3	12530	26633	225	75
CONTIGS600	24414212_c1_18	12531	26634	270	90
CONTIGS600	34430252_c2_20	12532	26635	210	70
CONTIGS600	111588_c3_24	12533	26636	381	127

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CONTIG5612	10048780_c2_14	12567	26670	345	115						
CONTIG5613	34569675_f1_2	12568	26671	183	61						
CONTIG5613	23626415_f2_8	12569	26672	186	62						
CONTIG5614	15710887_f1_4	12570	26673	264	88						
CONTIG5614	24221883_f2_5	12571	26674	228	76						
CONTIG5614	33399087_f2_6	12572	26675	189	63						
CONTIG5614	14972283_f2_9	12573	26676	339	113						
CONTIG5614	815667_c2_19	12574	26677	264	88						
CONTIG5615	2144752_f1_3	12575	26678	198	66						
CONTIG5615	6909383_f2_7	12576	26679	204	68						
CONTIG5615	36617136_f2_11	12577	26680	183	61						
CONTIG5615	6640686_f3_15	12578	26681	1497	499						
CONTIG5615	24892317_c3_24	12579	26682	186	62						
CONTIG5616	29320206_f2_8	12580	26683	405	135						
CONTIG5616	22283128_c1_19	12581	26684	201	67						
CONTIG5616	15902206_c1_21	12582	26685	255	85						
CONTIG5616	13785055_c2_28	12583	26686	294	98						
CONTIG5616	34553582_c2_30	12584	26687	258	86						
CONTIG5616	16600282_c2_31	12585	26688	507	169						
CONTIG5616	4709507_c3_34	12586	26689	765	255						
CONTIG5616	2750391_c3_35	12587	26690	336	112						
CONTIG5617	25626890_f2_3	12588	26691	339	113						
CONTIG5617	4704652_f3_5	12589	26692	1854	618						
CONTIG5618	23632877_f1_1	12590	26693	333	111						
CONTIG5618	23600042_c2_22	12591	26694	192	64						
CONTIG5618	25478377_c3_29	12592	26695	366	122						
CONTIG5619	7832_f1_4	12593	26696	195	65						
CONTIG5620	156461_f3_7	12594	26697	345	115						
CONTIG5620	24304587_c1_11	12595	26698	231	77						
CONTIG5620	23835902_c2_16	12596	26699	1182	394						
CONTIG5621	2756510_f1_1	12597	26700	249	83						
CONTIG5622	814152_c1_12	12598	26701	237	79						
CONTIG5623	20484630_c3_11	12599	26702	207	69						

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CONTIGS691	13016450_c3_31	12831	26934	261	87
CONTIGS693	2317_f1_3	12832	26935	195	65
CONTIGS693	10548275_c1_14	12833	26936	204	68
CONTIGS693	23594680_c2_17	12834	26937	759	253
CONTIGS693	34179000_c3_20	12835	26938	264	88
CONTIGS694	11114200_c1_14	12836	26939	249	83
CONTIGS694	22460938_c1_15	12837	26940	204	68
CONTIGS694	24645300_c1_16	12838	26941	528	176
CONTIGS694	33834677_c3_24	12839	26942	216	72
CONTIGS695	33319425_f1_1	12840	26943	237	79
CONTIGS695	4332180_f2_6	12841	26944	330	110
CONTIGS695	975027_f3_9	12842	26945	240	80
CONTIGS695	6542575_c2_12	12843	26946	216	72
CONTIGS695	6054687_c2_14	12844	26947	198	66
CONTIGS695	3301512_c3_16	12845	26948	192	64
CONTIGS696	2626925_f2_4	12846	26949	198	66
CONTIGS696	9788300_f3_7	12847	26950	210	70
CONTIGS696	9788312_c1_13	12848	26951	1038	346
CONTIGS697	11725056_f1_1	12849	26952	1179	393
CONTIGS697	10735301_f2_6	12850	26953	402	134
CONTIGS697	23632937_f3_8	12851	26954	279	93
CONTIGS697	31526957_f3_9	12852	26955	264	88
CONTIGS697	1986550_c1_15	12853	26956	198	66
CONTIGS697	6931677_c2_18	12854	26957	432	144
CONTIGS697	21753755_c2_20	12855	26958	369	123
CONTIGS697	26596928_c3_29	12856	26959	213	71
CONTIGS697	4018882_c3_30	12857	26960	186	62
CONTIGS698	14557812_f1_4	12858	26961	195	65
CONTIGS698	4022126_f1_5	12859	26962	225	75
CONTIGS698	6269068_f1_6	12860	26963	192	64
CONTIGS698	25656312_c1_17	12861	26964	381	127
CONTIGS698	6020801_c2_24	12862	26965	303	101
CONTIGS699	207943_c1_22	12863	26966	240	80

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CONTIG5778	14866507_f2_17	13161	27264	252	84
CONTIG5778	7054677_f3_20	13162	27265	210	70
CONTIG5778	5329752_f3_21	13163	27266	402	134
CONTIG5778	31798388_c3_31	13164	27267	207	69
CONTIG5779	11909650_c1_16	13165	27268	279	93
CONTIG5779	34089026_c2_18	13166	27269	207	69
CONTIG5780	3945932_f1_4	13167	27270	1083	361
CONTIG5780	42305_c2_26	13168	27271	201	67
CONTIG5781	23594525_f2_12	13169	27272	285	95
CONTIG5781	4079661_f3_14	13170	27273	198	66
CONTIG5781	4489510_f3_16	13171	27274	237	79
CONTIG5782	24414142_f2_9	13172	27275	210	70
CONTIG5782	29881928_c1_16	13173	27276	249	83
CONTIG5782	20367250_c2_19	13174	27277	675	225
CONTIG5782	1991625_c3_26	13175	27278	198	66
CONTIG5783	26015953_f1_3	13176	27279	183	61
CONTIG5783	24492187_f2_11	13177	27280	225	75
CONTIG5783	34266952_c1_27	13178	27281	720	240
CONTIG5783	25401900_c2_29	13179	27282	201	67
CONTIG5784	23600678_f1_2	13180	27283	198	66
CONTIG5784	26609383_f2_4	13181	27284	240	80
CONTIG5784	10313125_f3_11	13182	27285	192	64
CONTIG5784	992187_c1_15	13183	27286	213	71
CONTIG5784	21672813_c1_16	13184	27287	279	93
CONTIG5784	14147838_c2_18	13185	27288	222	74
CONTIG5784	14256252_c2_19	13186	27289	192	64
CONTIG5784	29304635_c3_27	13187	27290	216	72
CONTIG5784	6835150_c3_28	13188	27291	207	69
CONTIG5784	24304682_c3_29	13189	27292	255	85
CONTIG5785	2445312_f1_2	13190	27293	192	64
CONTIG5785	19955386_f2_9	13191	27294	420	140
CONTIG5785	23516316_f3_18	13192	27295	192	64
CONTIG5785	11797161_f3_20	13193	27296	342	114



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CONTIG5800	9929652_c3_10	13260	27363	192	64
CONTIG5800	3167325_c3_12	13261	27364	240	80
CONTIG5801	13753135_f2_7	13262	27365	504	168
CONTIG5801	29542502_f2_11	13263	27366	198	66
CONTIG5801	19726437_f2_15	13264	27367	192	64
CONTIG5802	24414062_f1_4	13265	27368	195	65
CONTIG5802	26199205_f1_5	13266	27369	204	68
CONTIG5802	22464087_f1_6	13267	27370	186	62
CONTIG5802	6136527_f1_9	13268	27371	252	84
CONTIG5802	16538432_f2_15	13269	27372	288	96
CONTIG5802	15032918_f2_16	13270	27373	342	114
CONTIG5802	110555383_c2_30	13271	27374	219	73
CONTIG5802	23844625_c2_35	13272	27375	189	63
CONTIG5802	2578200_c3_40	13273	27376	222	74
CONTIG5803	24394402_f1_1	13274	27377	195	65
CONTIG5803	21675010_f1_4	13275	27378	1092	364
CONTIG5803	5253762_c1_19	13276	27379	258	86
CONTIG5804	24634660_f1_5	13277	27380	492	164
CONTIG5804	24854681_f1_6	13278	27381	318	106
CONTIG5804	14846900_f1_7	13279	27382	651	217
CONTIG5804	24117250_f1_9	13280	27383	201	67
CONTIG5804	972155_f2_24	13281	27384	375	125
CONTIG5804	5865642_f3_33	13282	27385	216	72
CONTIG5804	26287555_c1_42	13283	27386	201	67
CONTIG5805	33395961_f2_9	13284	27387	276	92
CONTIG5805	35267811_c2_32	13285	27388	723	241
CONTIG5806	4875055_f2_11	13286	27389	519	173
CONTIG5806	5094087_f3_22	13287	27390	213	71
CONTIG5806	400453_c1_30	13288	27391	816	272
CONTIG5806	9859377_c2_36	13289	27392	897	299
CONTIG5806	4800125_c3_37	13290	27393	186	62
CONTIG5806	14267776_c3_39	13291	27394	276	92
CONTIG5806	20738825_c3_40	13292	27395	234	78







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CONTIG5821	24010290_f3_51	13392	27495	231	77
CONTIG5821	5331418_c1_60	13393	27496	261	87
CONTIG5821	679716_c1_63	13394	27497	192	64
CONTIG5821	25839417_c3_90	13395	27498	240	80
CONTIG5821	13799081_c3_91	13396	27499	264	88
CONTIG584	24022327_f3_2	13397	27500	192	64
CONTIG586	790700_f2_1	13398	27501	186	62
CONTIG587	25426626_f1_1	13399	27502	186	62
CONTIG587	2031950_f3_2	13400	27503	306	102
CONTIG590	878278_c2_2	13401	27504	225	75
CONTIG591	9802088_c2_1	13402	27505	822	274
CONTIG594	19725302_c3_3	13403	27506	210	70
CONTIG596	917192_c3_1	13404	27507	828	276
CONTIG597	2912636_f3_3	13405	27508	369	123
CONTIG599	20390713_f1_1	13406	27509	594	198
CONTIG60	24398512_c3_2	13407	27510	477	159
CONTIG600	26767788_c1_3	13408	27511	486	162
CONTIG601	13953301_f1_1	13409	27512	318	106
CONTIG604	4337838_f1_1	13410	27513	723	241
CONTIG605	24394500_c3_3	13411	27514	207	69
CONTIG610	16593790_c2_1	13412	27515	210	70
CONTIG613	36539193_c2_6	13413	27516	243	81
CONTIG618	14456500_c1_1	13414	27517	225	75
CONTIG619	9929787_c3_2	13415	27518	774	258
CONTIG62	6114387_f1_1	13416	27519	264	88
CONTIG620	9776885_f1_1	13417	27520	468	156
CONTIG625	21594051_f3_2	13418	27521	306	102
CONTIG626	4589833_f2_2	13419	27522	207	69
CONTIG627	23986387_f3_1	13420	27523	201	67
CONTIG63	25397187_f1_1	13421	27524	258	86
CONTIG630	2079125_c3_2	13422	27525	183	61
CONTIG632	21676692_c1_3	13423	27526	231	77
CONTIG633	4804056_f2_1	13424	27527	219	73

CONTIG634	10196957_f2_1	13425	27528	567	189						
CONTIG636	24304661_c1_1	13426	27529	204	68						
CONTIG637	12537506_c2_2	13427	27530	183	61						
CONTIG638	2393967_f3_3	13428	27531	324	108						
CONTIG641	24929650_f1_2	13429	27532	327	109						
CONTIG642	15815653_f2_2	13430	27533	243	81						
CONTIG642	4711677_c1_3	13431	27534	219	73						
CONTIG643	14459437_f1_1	13432	27535	750	250						
CONTIG644	15057966_c2_2	13433	27536	186	62						
CONTIG646	4328755_f1_1	13434	27537	492	164						
CONTIG646	31683142_f3_2	13435	27538	405	135						
CONTIG649	13782267_f1_1	13436	27539	285	95						
CONTIG649	1968750_c1_3	13437	27540	210	70						
CONTIG65	9957768_c3_2	13438	27541	402	134						
CONTIG654	35633543_f2_1	13439	27542	753	251						
CONTIG656	35792165_c2_5	13440	27543	198	66						
CONTIG657	13096905_f1_1	13441	27544	942	314						
CONTIG664	14562515_f1_1	13442	27545	777	259						
CONTIG665	984439_c2_3	13443	27546	204	68						
CONTIG666	25817187_f1_1	13444	27547	231	77						
CONTIG667	85180_c2_3	13445	27548	387	129						
CONTIG671	4181502_f1_1	13446	27549	384	128						
CONTIG671	13859385_c2_2	13447	27550	252	84						
CONTIG673	22457806_f2_1	13448	27551	339	113						
CONTIG673	4765693_c1_2	13449	27552	192	64						
CONTIG673	26359552_c3_3	13450	27553	240	80						
CONTIG678	24666031_f2_2	13451	27554	474	158						
CONTIG68	20392877_c3_2	13452	27555	249	83						
CONTIG680	117825_f2_1	13453	27556	186	62						
CONTIG681	24568811_f2_1	13454	27557	234	78						
CONTIG682	5157515_c1_1	13455	27558	354	118						
CONTIG682	23610062_c1_2	13456	27559	363	121						
CONTIG684	5282878_f3_1	13457	27560	195	65						

CONTIG684	24805442_c3_2	13458	27561	747	249
CONTIG686	9861317_f2_2	13459	27562	519	173
CONTIG692	23443842_c2_2	13460	27563	207	69
CONTIG693	26254813_c3_2	13461	27564	672	224
CONTIG694	31542708_f2_2	13462	27565	309	103
CONTIG694	240803_c3_3	13463	27566	459	153
CONTIG695	33714632_f2_2	13464	27567	204	68
CONTIG695	4068952_c2_3	13465	27568	258	86
CONTIG696	23910911_f3_3	13466	27569	192	64
CONTIG697	30469637_c1_3	13467	27570	246	82
CONTIG698	31683333_c1_2	13468	27571	360	120
CONTIG702	32041015_f1_1	13469	27572	210	70
CONTIG706	29690708_c3_4	13470	27573	201	67
CONTIG715	21907838_c1_2	13471	27574	348	116
CONTIG716	6019765_c3_5	13472	27575	576	192
CONTIG717	15675925_f3_1	13473	27576	369	123
CONTIG719	35189186_c3_3	13474	27577	189	63
CONTIG721	26257936_c1_2	13475	27578	195	65
CONTIG721	161267_c3_4	13476	27579	240	80
CONTIG725	24414555_c2_2	13477	27580	234	78
CONTIG727	24398463_c3_3	13478	27581	198	66
CONTIG729	36111012_c1_1	13479	27582	426	142
CONTIG732	6046883_c3_4	13480	27583	183	61
CONTIG733	34187765_f1_2	13481	27584	279	93
CONTIG733	16410912_c2_3	13482	27585	381	127
CONTIG736	965_f3_1	13483	27586	696	232
CONTIG739	24313191_c3_1	13484	27587	420	140
CONTIG74	22304787_c2_2	13485	27588	213	71
CONTIG740	35719443_f1_1	13486	27589	633	211
CONTIG741	14625311_f2_2	13487	27590	333	111
CONTIG741	29339662_f3_3	13488	27591	510	170
CONTIG742	25595183_f1_1	13489	27592	489	163
CONTIG743	26204625_f1_1	13490	27593	192	64







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b2x 6278.x	3363200_f3_3	13689	27792	723	241				
b2x 6264.y	2141053_c3_5	13690	27793	378	126				
b9x 3603.x	29468785_f2_1	13691	27794	297	99				
b1x 3303.y	33229666_f1_1	13692	27795	339	113				
b9x 3602.x	30163187_f1_1	13693	27796	477	159				
b2x 6118.x	24298502_c2_2	13694	27797	198	66				
b9x 3189.x	23860912_f2_1	13695	27798	228	76				
b9x 3147.y	14922067_f3_3	13696	27799	309	103				
b9x 3689.y	12704410_c1_3	13697	27800	417	139				
b9x 3670.x	23837513_c2_2	13698	27801	225	75				
b9x 3618.y	5281661_c3_5	13699	27802	201	67				
b9x 3618.y	35188762_c3_6	13700	27803	222	74				
b1x 8436.y	1006406_f3_1	13701	27804	201	67				
b9x 3d35.x	30364566_f1_1	13702	27805	585	195				
b9x 3d16.y	6348880_f1_1	13703	27806	216	72				
b9x 3d16.y	22062812_c3_3	13704	27807	528	176				
b9x 3d08.x	956580_c3_4	13705	27808	255	85				
b9x 3c92.x	5360383_f1_1	13706	27809	192	64				
b2x 6057.x	4726536_f2_1	13707	27810	603	201				
b9x 3c06.y	11915925_f2_2	13708	27811	186	62				
b9x 3c06.y	30265928_c3_4	13709	27812	183	61				
b1x 8443.x	22558255_f3_1	13710	27813	492	164				
b1x 8443.x	35969633_c3_3	13711	27814	243	81				
b2x 5980.y	33644630_c3_3	13712	27815	564	188				
b9x 3d50.x	4348957_f2_1	13713	27816	204	68				
b9x 3872.y	15626282_c1_2	13714	27817	189	63				
b9x 3854.y	21883437_f1_1	13715	27818	498	166				
b9x 3854.y	6510906_f2_2	13716	27819	261	87				
b1x 8485.x	4000338_c3_1	13717	27820	432	144				
b9x 3665.x	10009626_c3_1	13718	27821	627	209				
b9x 3527.y	19694066_c2_4	13719	27822	246	82				
b2x 5766.x	6835838_f3_3	13720	27823	333	111				
b2x 5766.x	35209750_c1_4	13721	27824	219	73				

b2x15766.x	25432825_c3_5	13722	27825	261	87
b9x13491.x	5984467_f1_2	13723	27826	219	73
b9x13491.x	29487557_c3_3	13724	27827	933	311
b2x15753.y	25985317_f2_1	13725	27828	534	178
b9x13380.x	1062693_f1_1	13726	27829	435	145
b9x13319.y	35156537_c1_2	13727	27830	258	86
b2x15753.x	14492337_f2_3	13728	27831	333	111
b9x13249.x	12268763_f1_1	13729	27832	600	200
b9x12269.x	4456550_f2_1	13730	27833	501	167
b9x12987.y	31407053_f3_1	13731	27834	492	164
b2x15727.x	4880140_c2_1	13732	27835	210	70
b9x12w88.x	829378_f1_1	13733	27836	195	65
b9x12w88.x	21493761_f2_2	13734	27837	327	109
b9x12w72.x	10350061_c1_4	13735	27838	510	170
b9x12w68.x	24697555_c3_5	13736	27839	387	129
b9x12v46.x	16531686_c2_1	13737	27840	480	160
b2x15689.y	33258342_c2_3	13738	27841	189	63
b9x12v30.x	24318817_c3_2	13739	27842	345	115
b9x12u82.x	32225837_f2_1	13740	27843	243	81
b1x10645.x	4775286_c2_4	13741	27844	204	68
b9x12u61.y	5314677_f3_1	13742	27845	261	87
b1x13827.x	23882951_c3_2	13743	27846	195	65
b9x12u17.y	471040_f2_1	13744	27847	507	169
b9x12u47.y	13023593_c2_8	13745	27848	327	109
b9x12u15.y	34573957_c2_6	13746	27849	237	79
b9x12u15.y	24026578_c2_7	13747	27850	204	68
b9x12q68.y	16408442_f3_2	13748	27851	711	237
b9x12n61.x	3157180_f3_2	13749	27852	588	196
b9x12n61.x	4892127_c3_5	13750	27853	306	102
b9x12n34.y	10600307_f3_1	13751	27854	198	66
b2x15645.y	24016567_f1_1	13752	27855	375	125
b2x15645.y	957827_f2_2	13753	27856	390	130
b2x15645.y	2924177_c2_4	13754	27857	360	120

b2x15632.y	4694377_c1_2	13755	27858	363	121				
b2x15632.y	4864211_c2_3	13756	27859	507	169				
b9x12k65.x	5282802_f1_1	13757	27860	582	194				
b9x12k65.x	3927008_c2_2	13758	27861	225	75				
b2x15443.x	6094632_f1_1	13759	27862	183	61				
b2x15443.x	24801342_f2_2	13760	27863	198	66				
b2x15443.x	2166042_f3_3	13761	27864	192	64				
b9x12h24.x	13880181_f3_1	13762	27865	621	207				
b9x12h24.x	25630378_c3_3	13763	27866	327	109				
b9x12i56.y	21658462_f2_1	13764	27867	231	77				
b9x12d49.y	23632187_c2_1	13765	27868	690	230				
b2x15502.x	4031638_c1_1	13766	27869	582	194				
b2x15473.x	25586075_c1_1	13767	27870	339	113				
b9x12989.y	806599_c1_2	13768	27871	192	64				
b9x12884.x	5979140_c2_3	13769	27872	183	61				
b9x12850.y	36537580_f1_1	13770	27873	192	64				
b9x12850.y	10945200_f2_3	13771	27874	420	140				
b9x12850.y	1225305_c2_6	13772	27875	249	83				
b9x12776.y	24020312_c1_4	13773	27876	240	80				
b9x12776.y	34429652_c2_5	13774	27877	372	124				
b2x12886.x	2437665_c2_3	13775	27878	195	65				
b2x12886.x	25428135_c3_4	13776	27879	303	101				
b9x12658.y	24801561_f1_1	13777	27880	204	68				
b9x12636.y	22296875_c1_2	13778	27881	189	63				
b9x12636.y	1174186_c1_3	13779	27882	183	61				
b9x12591.x	2394167_f1_1	13780	27883	585	195				
b9x12387.y	13944050_f1_1	13781	27884	267	89				
b2x12835.y	1289280_f2_1	13782	27885	570	190				
b9x12220.x	22267813_c2_2	13783	27886	201	67				
b2x12829.x	36382002_f2_1	13784	27887	198	66				
b9x11y56.y	14454757_c2_2	13785	27888	474	158				
b9x11x80.x	31683200_c1_1	13786	27889	255	85				
b1x18647.x	24008386_c1_1	13787	27890	444	148				





b9x11954.y	4006930_c1_5	13821	27924	474	158
b9x11910.y	15735002_f3_2	13822	27925	213	71
b9x11910.y	21678402_c2_3	13823	27926	234	78
b9x11677.x	24413962_c2_3	13824	27927	228	76
b9x11364.y	10001557_f3_1	13825	27928	288	96
b9x11233.y	34199187_c1_3	13826	27929	219	73
b9x11209.x	390755_f3_2	13827	27930	231	77
b9x11209.x	35214067_c2_3	13828	27931	309	103
b9x11203.y	4082031_f2_1	13829	27932	228	76
b9x11203.x	10977127_c2_2	13830	27933	348	116
b9x11160.x	10945950_c1_5	13831	27934	255	85
b9x11137.x	3235386_f3_1	13832	27935	378	126
b9x11074.x	26384712_c1_2	13833	27936	186	62
b9x11044.y	25875430_c2_6	13834	27937	789	263
b9x10y60.x	4688952_f3_2	13835	27938	201	67
b9x10w84.y	1203125_c3_2	13836	27939	462	154
b9x10v59.x	22848532_c2_2	13837	27940	216	72
b9x10v30.y	23548425_c3_2	13838	27941	360	120
b1x18786.x	24414132_c1_2	13839	27942	261	87
b9x10u31.x	6412687_f3_1	13840	27943	192	64
b9x10r79.x	15627_f2_1	13841	27944	318	106
b9x10r79.x	30663212_c2_2	13842	27945	219	73
b9x10t19.x	4890713_f3_1	13843	27946	870	290
b2x11969.y	33469040_f3_1	13844	27947	210	70
b2x11959.y	25413263_c3_2	13845	27948	516	172
b9x10p88.x	24870777_f3_1	13846	27949	567	189
b1x18823.x	5275337_c1_1	13847	27950	243	81
b2x13860.y	22863178_c3_2	13848	27951	189	63
b9x10j44.x	428192_f1_1	13849	27952	420	140
b2x11862.y	16925255_f2_1	13850	27953	531	177
b2x13867.y	6485916_f2_1	13851	27954	198	66
b9x10g01.y	2000141_f2_1	13852	27955	192	64
b2x11832.y	3910156_f2_1	13853	27956	516	172

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b4x10393.x	14100932_c2_2	13887	27990	621	207
b4x10274.y	35238387_c1_2	13888	27991	333	111
b4x10106.x	36132087_c1_4	13889	27992	645	215
b3x19646.y	885386_f2_1	13890	27993	246	82
b3x19646.y	14953427_c2_2	13891	27994	186	62
b3x19605.y	5350325_c2_2	13892	27995	186	62
b3x19517.y	30504813_c3_5	13893	27996	228	76
b2x11002.y	5338561_f3_2	13894	27997	606	202
b3x19470.y	5116406_f1_1	13895	27998	183	61
b3x19283.y	36385062_f1_1	13896	27999	384	128
b3x19243.x	32632974_c1_4	13897	28000	213	71
b3x19234.y	28800030_f3_1	13898	28001	186	62
b1x11554.y	23623305_f3_1	13899	28002	387	129
b1x11554.y	13703450_c1_2	13900	28003	420	140
b3x18982.x	4725030_c1_4	13901	28004	225	75
b3x18807.y	4038442_f3_1	13902	28005	267	89
b3x18737.y	781250_c1_2	13903	28006	657	219
b3x18642.x	29410681_c3_3	13904	28007	411	137
b3x18592.x	2048755_f1_1	13905	28008	405	135
b3x18592.x	4453127_f3_2	13906	28009	192	64
b2x10717.x	23718765_f2_1	13907	28010	489	163
b3x17956.y	21746013_c3_3	13908	28011	501	167
b3x17714.x	26562500_c1_1	13909	28012	324	108
b3x17684.y	15735155_f3_2	13910	28013	183	61
b3x17370.x	4568762_f2_1	13911	28014	441	147
b3x17064.y	4821950_f1_1	13912	28015	459	153
b3x16962.y	23476425_f1_1	13913	28016	207	69
b3x16871.y	3907783_f1_1	13914	28017	486	162
b2x14264.y	1048312_c1_2	13915	28018	207	69
b3x16673.x	291663_f2_1	13916	28019	648	216
b3x16673.x	13939087_f2_2	13917	28020	243	81
b1x19249.x	433332_f1_1	13918	28021	579	193
b1x19249.x	2112877_c2_2	13919	28022	234	78

b2x10230.x	9782967_f3_1	13920	28023	207	69						
b3x16529.y	22447260_f3_1	13921	28024	231	77						
b3x16483.x	23709678_c3_3	13922	28025	309	103						
b1x19259.x	21520002_c3_1	13923	28026	765	255						
b3x16120.y	35807758_f1_1	13924	28027	498	166						
b3x16113.x	24415637_c2_2	13925	28028	234	78						
b3x16093.y	16532836_c1_4	13926	28029	246	82						
b3x16089.y	15103550_f1_1	13927	28030	765	255						
b3x16083.y	5337801_f1_1	13928	28031	198	66						
b3x16069.y	22150053_c2_3	13929	28032	222	74						
b3x16067.y	11180135_f1_1	13930	28033	204	68						
b3x16067.y	29690641_f2_2	13931	28034	240	80						
b3x16062.y	4176290_c1_1	13932	28035	213	71						
b3x16061.y	5942261_c1_5	13933	28036	348	116						
b3x16058.y	5370182_f2_2	13934	28037	399	133						
b3x16054.y	26850392_f2_1	13935	28038	207	69						
b3x16050.y	6723214_c1_3	13936	28039	183	61						
b3x16050.y	12125043_c2_4	13937	28040	222	74						
b3x16048.y	1175375_c2_4	13938	28041	210	70						
b1x11921.y	29564002_c1_2	13939	28042	183	61						
b3x16046.y	26692801_f1_1	13940	28043	189	63						
b3x16043.y	24025288_f2_3	13941	28044	279	93						
b3x16043.y	30277288_c2_6	13942	28045	270	90						
b3x16042.y	32243965_f3_3	13943	28046	240	80						
b3x16041.x	478166_f3_1	13944	28047	189	63						
b3x16039.y	23915660_f1_1	13945	28048	258	86						
b3x16039.y	480436_c1_3	13946	28049	195	65						
b3x16035.y	29334635_f3_4	13947	28050	249	83						
b3x16035.y	36598936_c2_6	13948	28051	231	77						
b3x16032.y	19631632_f1_1	13949	28052	660	220						
b1x11963.y	23603442_f1_1	13950	28053	192	64						
b1x11963.y	9853430_f1_2	13951	28054	603	201						
b1x11963.y	4766385_c2_5	13952	28055	207	69						

b3x 6011.y	326 0410_f1_1	13953	28056	186	62
b1x 1972.x	2193758_c1_2	13954	28057	846	282
b3x 6010.y	4193933_f3_2	13955	28058	285	95
b1x 1984.y	36525947_f3_3	13956	28059	861	287
b3x 6005.y	11062677_c2_4	13957	28060	225	75
b3x 6004.y	31698941_f1_1	13958	28061	240	80
b3x 6002.y	32518761_f3_4	13959	28062	270	90
b3x 5960.y	29296925_c3_2	13960	28063	258	86
b3x 5773.y	7157826_c1_2	13961	28064	210	70
b3x 5701.x	24422152_c3_2	13962	28065	465	155
b3x 5687.x	23486632_c3_2	13963	28066	543	181
b3x 5661.y	191038_f2_1	13964	28067	246	82
b1x 9595.y	208325_f2_1	13965	28068	591	197
b9x 3.v91.x	14570262_f1_1	13966	28069	246	82
b3x 5457.y	34027307_g3_1	13967	28070	561	187
b1x 4536.y	5088533_f1_1	13968	28071	504	168
b3x 5367.x	16663391_f3_1	13969	28072	219	73
b3x 5361.x	14563885_f3_1	13970	28073	357	119
b3x 5328.x	24303812_f1_1	13971	28074	264	88
b1x 4543.y	9812625_c2_2	13972	28075	201	67
b1x 4543.y	274082_c3_3	13973	28076	312	104
b2x 4358.y	10985075_f2_1	13974	28077	231	77
b1x 4555.y	5914687_c1_1	13975	28078	261	87
b1x 4555.y	26367630_c2_2	13976	28079	255	85
b3x 5141.y	2150800_c1_1	13977	28080	189	63
b3x 5121.y	3955377_f2_1	13978	28081	201	67
b3x 5082.x	29334842_f1_1	13979	28082	210	70
b3x 4944.x	23554625_c2_1	13980	28083	522	174
b1x 4905.y	21878843_f1_1	13981	28084	504	168
b1x 4919.x	2010414_f1_1	13982	28085	186	62
b3x 4811.x	21657636_c2_2	13983	28086	204	68
b3x 4807.x	22445181_c3_5	13984	28087	510	170
b1x 4928.x	6359842_c2_3	13985	28088	183	61

b1x14936.x	13143782_f3_1	13986	28089	570	190						
b1x15013.x	13830301_c3_1	13987	28090	189	63						
b1x12474.x	3140777_c3_2	13988	28091	195	65						
b3x14569.x	861627_c2_1	13989	28092	267	89						
b2x13268.x	34117127_c1_1	13990	28093	192	64						
b2x13268.x	25823437_c2_2	13991	28094	276	92						
b3x14433.y	21538877_c1_3	13992	28095	441	147						
b2x14441.y	24406937_f2_2	13993	28096	390	130						
b3x14418.y	22837578_f3_4	13994	28097	297	99						
b1x12521.y	33382282_c1_2	13995	28098	690	230						
b3x14292.y	662887_f1_1	13996	28099	213	71						
b1x15077.y	4101562_c2_3	13997	28100	288	96						
b3x14239.y	9805406_f1_1	13998	28101	393	131						
b1x15145.y	188385_c1_1	13999	28102	645	215						
b1x14330.x	4415937_c2_1	14000	28103	360	120						
b3x13926.x	14143762_f2_1	14001	28104	204	68						
b3x13893.x	22673766_f3_1	14002	28105	351	117						
b1x15375.x	585811_f2_1	14003	28106	402	134						
b1x15375.x	15762_c3_4	14004	28107	360	120						
b3x13751.y	22266893_c1_3	14005	28108	810	270						
b3x13728.x	4564752_c2_1	14006	28109	264	88						
b1x15451.x	14335937_f2_1	14007	28110	207	69						
b3x13525.x	24397802_c2_1	14008	28111	213	71						
b3x13430.x	34111378_f3_3	14009	28112	186	62						
b3x13315.y	20334687_f1_1	14010	28113	288	96						
b3x13305.y	23625187_f2_1	14011	28114	198	66						
b3x13305.y	24414633_c3_4	14012	28115	198	66						
b3x13296.y	36584432_c2_2	14013	28116	480	160						
b2x14580.y	10657512_c2_1	14014	28117	561	187						
b1x15611.x	14845125_f3_1	14015	28118	192	64						
b2x14584.x	14453557_c2_2	14016	28119	387	129						
b3x13229.x	6024000_c2_1	14017	28120	204	68						
b3x13227.y	23836406_f1_1	14018	28121	240	80						

[illegible]

b2x 9077.y	7126905_f1_2	14052	28155	264	88
b2x 9038.x	23475676_f2_1	14053	28156	465	155
b2x 8992.y	20113392_f1_1	14054	28157	186	62
b1x 7289.y	19923126_f2_1	14055	28158	192	64
b1x 7289.y	16578765_c2_2	14056	28159	198	66
b1x 7289.y	33314438_c3_3	14057	28160	195	65
b2x 8774.y	21486017_f1_1	14058	28161	321	107
b2x 8614.y	7156558_f3_1	14059	28162	654	218
b1x 2896.y	16900755_f1_1	14060	28163	627	209
b2x 8564.y	26842204_f2_1	14061	28164	369	123
b1x 2915.y	9845035_f2_1	14062	28165	183	61
b2x 8561.y	4901878_f2_1	14063	28166	270	90
b2x 8550.y	23865802_c1_3	14064	28167	216	72
b1x 7564.y	24339078_f2_1	14065	28168	228	76
b1x 7564.y	6831678_f3_2	14066	28169	297	99
b1x 7564.y	1990880_c3_3	14067	28170	201	67
b1x 7567.y	19970192_f1_1	14068	28171	198	66
b2x 8389.x	24851537_f1_1	14069	28172	390	130
b1x 7708.y	642665_f3_1	14070	28173	468	156
b2x 8370.y	32204787_f1_1	14071	28174	528	176
b2x 8261.y	22461532_f1_1	14072	28175	285	95
b1x 7784.y	6700_c3_1	14073	28176	210	70
b2x 8181.y	32609552_f1_1	14074	28177	576	192
b2x 8172.x	22454432_f1_2	14075	28178	429	143
b2x 8172.x	14096936_c2_4	14076	28179	279	93
b1x 4078.y	127_c2_1	14077	28180	183	61
b1x 3049.y	2776442_c3_2	14078	28181	570	190
b2x 8152.x	578437_f2_3	14079	28182	192	64
b1x 7788.y	32454675_f2_1	14080	28183	714	238
b2x 8065.x	11735267_f2_1	14081	28184	219	73
b2x 8056.x	33634562_f1_1	14082	28185	516	172
b2x 8053.x	16835943_f2_1	14083	28186	276	92
b1x 7830.y	33259813_c3_1	14084	28187	306	102



b2x17956.x	30267327_f2_1	14085	28188	183	61					
b2x17871.y	34181300_f1_1	14086	28189	183	61					
b2x17871.y	24414057_c3_2	14087	28190	402	134					
b2x17864.x	20595816_c2_1	14088	28191	489	163					
b2x14964.y	470641_f3_1	14089	28192	780	260					
b2x17609.y	25422252_f1_1	14090	28193	207	69					
b1x17954.y	34618753_c3_4	14091	28194	540	180					
b1x17976.y	20046901_f1_2	14092	28195	354	118					
b1x17976.y	23594000_c1_3	14093	28196	252	84					
b2x17388.y	7079206_f2_1	14094	28197	456	152					
b2x17371.y	4812501_f2_1	14095	28198	282	94					
b2x17371.x	14569682_c3_2	14096	28199	504	168					
b2x17301.y	4171903_c2_1	14097	28200	243	81					
b2x17276.y	48440902_f2_2	14098	28201	507	169					
b2x17229.x	10580253_c2_4	14099	28202	204	68					
b2x15106.y	25586442_f3_1	14100	28203	189	63					
b2x15106.y	4885965_c2_2	14101	28204	348	116					
b2x17138.y	32628776_f2_1	14102	28205	537	179					
b2x15171.y	24329705_f2_1	14103	28206	195	65					